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SUMMARIES

A65720 Sequence 1	A65720	5	2679	72.8	77.2	24
x94608 C.familiari	CFB2AR	w	1948	72.8	77.2	23
U73206 Canis famil	CFU73206	w	1298	72.8	77.2	22
286037 B.taurus mR	BTB2ADREC	w	2032	74.3	78.8	21
X15643 Mouse gene	MMB2ARG	12	4928	75.8	80.4	20
L39264 Rattus norv	RATMTA	12	4197	75.8	80.4	19
-	RSB2AR	12	4190	75.8	80.4	18
J03024 Rat beta-ad	RATADBC	12	1959	75.8	80.4	17
	PIGB2AR	w	5288	78.9	83.6	16
AF192345 Felis cat	AF192345	w	1536	78.9	83.6	15
Caca	MACB2AR	=	1320	90.9	96.4	14
AC011334 Homo sap	AC011334	43	134419	97.0	102.8	13
AC011354 Homo sap	AC011354	43	132858	97.0	102.8	12
X04827 Human mRNA	HSBARR	9	1970	97.0	102.8	1
J02960 Human beta	HUMADRBRA	10	3458	98.5	104.4	10
AF203386 Homo sap	AF203386	39	1290	98.5	104.4	9
AF169225 Homo sap1	AF169225	39	1290	98.5	104.4	æ
AF022955 Homo sap	AF022955	11	1242	98.5	104.4	7
AF022954 Homo sap	AF022954	11	1242	98.5	104.4	σ
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AF202305 Homo sap	AF202305 .	<u>د</u>	1286	99.6	105.6	4
M15169 Human beta	HUMADRBR	10	3451	100.0	106	w
Y00106 Human gene	HSBAR	9	2305	100.0	106	2
AF022956 Homo sap1	AF022956	11	1242	100.0	106	1
Description	ID	. BB	Match Length	Match	Score	No.

Source Licinati, OH 45267-0564, USA Source Licinati, OH 45267-0564, USA 9ene / Organism="Homo Sapiens" 1.1242	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; UTHERS Reihsaus, P. Indres; Catarrhini; Hominidae; Homo. DURNAL In normal and astimatic subjects REBROE 2 (bases 1 to 1242) PIRES A POLYMORPHISM OF the beta 2-adrener REBROE 2 (bases 1 to 1242) FOURTH Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Cell Mol. Biol. 8 (3), 344-339 (1993) FOURTH AM. J. Respir. Secuptor SIGE A POLYMORPHISM OF the human beta 2-adrener and 1 J. Biol. Les of the receptor since (bases 1 to 1242) FOURTH AM. J. Respir. Secuptor Signal Amorthesis of the Human beta 2-adrener and 1 Respirate Advance of the human beta 2-adrener and 1 Respirate Advance of the human beta 2-adrener and 1 Respirate Advance of the Human beta 2-adrener and 1 Respirate of 1 Advance of 1 A	26 72.4 68.3 2018 12 MAARBR 27 35.2 38.9 3780 12 MAARBR 28 35.2 33.2 3390 12 MAARBR 28 35.2 33.2 16951 2 MSU46848 29 33.6 31.7 17584 50 MSU46848 30 33.6 31.7 17584 50 MSU46848 31 31.4 20.5 34893 15 SC17 32 32.8 30.9 241454 78 MC025353 35 30 28.3 4720 42 MC03576 30 28.3 4720 42 MC03576 30 28.3 3720 42 MC03976 30 28.3 139723 51 AC01070 11 30 28.3 139723 51 AC010970 12 30 28.3 139723 51 AC010970 13 30 28.3 139723 51 AC010973 14 30 28.3 29.88 51 AC010938 29.8 28.1 12938 34 AE003733 29.8 28.1 29.88 34 AE003525 29.8 28.1 1330 2 AE001888 29.2 27.5 19791 1 SPFKBAD NAF022956 ON Homo saptiens beta2-addres DNA AF022956
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and Lefkowitz,R.J.

cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor platelet-derived growth factor Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
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Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,

Dixon,R.A., Keller,P., Caron,M.G. and Lefkowltz,R.J.

Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
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B7222338
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Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
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1369. .3383
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Ruperr, J.L. and Hochachka, P.W.
Beta-2-adrenergic receptor allele frequencies in two
Direct Submission
Submitted (04-NOV-1999) Zoology, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 124, Canada
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1603 AACGGCAGCGCCTTCTTGCTGGCACCCAATAGAAGCCATGCGCCGGACCACGACGTCACG 1662
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                                                                                    Amino-terminal polymorphisms of the human beta 2-adro
receptor impart distinct agonist-promoted regulatory
Biochemistry 33 (32), 9414-9419 (1994)
                                                                                                                                                                                                 properties of the receptor J. Biol. Chem. 268 (31). 2
                                                                                                                                                                                                                            Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1242)
Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic in normal and asthmatic subjects
Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
4 (bases 1 to 1242)
Liggett, S.B. and Gre
                                  Erratum:[[published erratum 29;33(47):14368]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens beta2-adrenergic receptor AF022953
                                                                                                                                         Green, S.A., Turki, J.,
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TVPSDNIDSQGRNCSTNDSLL"
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/protein_id="AAF17569.1"
/db_xref="01:6573153"
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/chromosome="5"
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                                                                                                                                         Innis, M. and Liggett, S.B.
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                                                                                                             Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor properties. Chem. 268 (31), 23116-23121 (1993)
Green, S.A., Turki, J., Innis, M. and Liggett, S.B. Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
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Mutations in the gene encoding for the beta 2-adrenergic receptor
in normal and asthmatic subjects
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Submitted (04-SEP-1997) Medicine, Univ of Cincinnati,
Ave ML670564, Cincinnati, OH 45267-0564, USA
Location/Qualifiers
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/product="beta2-adrenergic receptor"
/protein_id="AAB82148.1"
/db_xref="GI:2570527"
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Liggett,S.B. and Green,S.A.
Direct Submission
Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor J. Biol. Chem. 268 (31), 23116-23121 (1993)
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
Mutations in the gene encoding for the beta 2-adrenergic recein normal and asthmatic subjects
in normal and asthmatic subjects
in normal and asthmatic subjects
in sespir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/replace="c"
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory properties Biochemistry 33 (32), 9414-9419 (1994)
94347707
2 (bases 1 to 1290)
Rupert, J.R. and Hochachka, P.W.
Direct Submission
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Submitted (04-SEP-1997) Medicine, Univ of Cincinnati,
Ave ML670564, Cincinnati, OH 45267-0564, USA
                                                                                                                 Rupert, J.R. and Hochachka, P.W.
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1290)
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Liggett, S.B. and Green, S.A.
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29;33(47):14368]]
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Homo sapiens beta-2 adrenergic receptor (ADRB2) gene, complete cds.
AF203386
AF203386.1 GI:6636495
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                                                                                                                                      Submitted (09-NOV-1999) Zoology, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                          Rupert, J.L. and Hochachka, P.W.
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/note="isolated from a Quechua speaking
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Emorine, L.J., Marullo, S., Delavier-Klutchko, C., Kaveri, S.V.,
Durieu-Trantmann, O. and Strosberg, A.D.
Structure of the gene for human beta 2-adrenergic receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adrenergic receptor; beta-2 adrenergic receptor. Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and promoter characterization Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6
                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable copy provided by L.J.Emorine, 25-AUG-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                      88041037
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                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="H-beta-R-[9,10,11]."
/cell_line="A431"
/tissue_type="epidermis"
/map="5q31-q32"
277. .1032
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/db_xref="G1:6636496"
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/translation="McGPGNGSAFILAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
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LAIVFGNVLVITAIAKFERLQTVINYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
MWCEEWTSIDVLCVTASIETLCVIAVGTATTSPEXYQSLIKNKARAVIILMVGV
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAGSIVSFYVPLVIMVFV
YSRVFQEAKRQLQKINKSEGREHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLMWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
/translation="MfereyTglpGvcWegsIISARVRQVRSTQMETSVSVSLWMPPS
GRVFTGCVCHHVFVLLGASVFYSGRVSYLDRGDFVPDGGTVRAEASVHVGELGGCVSV
SMAVVRYKSEHVCQGVFVPVCACLGGHSRFLFNVGQCRCAALCLETSSRAGAQGRQVA
ATEEPKAPGLACKHTTSSFSPLGPARVAGKQWMPALQGAVGPRFGQPQEKEGEGRGGK
GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
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26. .1267
                                                                                                  /product="unknown protein"
/protein_id="AAA88016.1"
/db_xref="GI:560762"
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1. .3458
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                                                                                                                                                                                 /note="ORF; putative"
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al Similarity 99.1%;
105; Conservation
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1 (bases 1 to 1970)
Chung, F. Z., Lentes, K. U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A. R., Fraser, C. M. and Venter, J. C. Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 bp upstream of EcoRI site; chromosome 5q31-q32.
                                                                                                                            Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases substantial corrections are reported in [2] Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                                       Kerlavage, A.R.
Direct Submission
                                                                                                                                                                                                                                                                beta-receptors and porcine muscarinic receptors FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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TVPSDNIDSQGRNCSTNDSLL"
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                     /clone_lib="neonatal human brain stem"
178. .1419
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/codon_start=1
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1264. .2505
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1064. .3057
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1055. .3057
/note-"beta-adrenergic receptor (AA 1-413)"
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/db_xref="taxon:9606"
                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 cagcaaagggacgaggtggtgggtggtgggcatgggcatcgtcatgt 106
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                                *NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 132858)
DOE Joint Genome Institute.
                                                                                                                                                                                             Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
* by the finished sequence as soon as it is available and * the accession number will be preserved.
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HTG; HTGS_PHASE2; HTGS_DRAFT
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                                                                                                                                                                                                                                     Direct Submission
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DOE Joint Genome Institute.
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Laivegnylvitaiakferlofytnyfitslacadlynglavypfgaahiilmkmyteg
Nfwcefwtsidvlcytasietlcytavdryfaitspekygslitknkarviiilmyniy
Sgltselpighhwyrathdealncyametccdeftngafafassiysfeydlylmyfy
YSRVFQEAKRQLQKIDKSEGRFHYONLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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/db_xref="GI:29373"
/db_xref="SWISS-PROT:P07550"
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Pred. No. 3.9e-16;
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Local Similarity 98.1%;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134419)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-OCT-1999) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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DOE Joint Genome Institute.
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                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 134419: contig of 134419 bp in length.
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/db_xref="taxon:9606"
/chromosome="5"
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26539 c 25722 g 40476 t
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                   /clone="CIT-HSPC_235N17"
28042 c 27433 g 3867
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gap of unknown length
60531: contig of 59370 bp in length
gap of unknown length
132858: contig of 72327 bp in length
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 Score 102.8; DB 43;
Pred. No. 1.9e-16;
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Pred. No. 1.9e-16;
0; Mismatches 2
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Amend, A.M. and Guan, X.M.
Cloning, sequencing, and expression of the
adrenergic receptor
DNA Cell Biol. 14 (9), 753-757 (1995)
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Macaca mulatta cDNA to
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Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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                                                                                                                                                                                                                                                                                                                                  /product="beta-2 adrenergic receptor"
/protein_id="AAC41914.1"
/protein_id="AAC41914.1"
/db_xref="GI:1004339"
/db_xref="GI:1004339"
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LAIVEGNVLVITAIAKEERLQTVTNYFITSLACADLVMGLAVVPFQAAHILAKNWTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPKYQSLITKNKARVILLAVWFV
SGLTSFLPIQMWYRATHQEAINCYAKETCCDFFTNQAYAHASSIVSFYVPLVIMVFV
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QGTYPSDNIDSQGRSCSTNDSLL"
1289. 1320
/gence"B2AR"
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/note="genomic DNA for this receptor sequenced and
to be identical with the cDNA"
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                                                                                                                                                                                                                                                                                                      IIMGTETLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSGENPLIYCRSPDFRI
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Best Local Similarity 86.8%;
Matches 92; Conservative
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1 (bases 1 to 1336)

Cully,D.F., Tremml,G. and Zachwieja,S.
Felia domesticus beta adrenergic receptor subtype 2
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Cully, D.F., Tremml, G. and Zachwieja, S.
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IIMGTFTLCWLPFFIVNIYHVIQDNLIPKEVYILLNMVGYVNSAFNPLIYCRSPDFRI
AFQELLCLRSSLKAYKGMYSNINSUSRTDYAGEHSGGPLGQEKDSEVLCEDPPGTENL
ANRQGTVPNDSIDSQGQNGSTNDSLL"
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/protein_id="AAF04304.1."
/protein_id="AAF04304.1."
/db_xrcf=-01:6120129"
/translation="MG0PGNRSVFLLAPNGSHAPDQDGTQERNDAWVGMGIVMSLIV
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/translation="
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receptor subtype 2"
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/db_xref="taxon:9685"
/note="synonym: Felis domesticus"
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Pred. No. 2.2e-11;
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Post-processing: Minimum Match 0%
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02-OCT-1997, J00982,
24-MAR-1996; JP-072914.
(DAIN ) DAINIPPON PHARM CO LTD.
(UDII K, Furutani Y, Kawashima H
WPI; 97-489627/45.
P-PSDB; W34320,
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Homo sapiens.
Key
CDS
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CDS
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                                                                              21-DEC-1998 (first entry)
Human beta-2-adrenergic receptor
Beta-2-adrenergic receptor; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Disclosure; Page 27-30; 47pp; Japanese.

This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
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20-APR-1998 (first entry)
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problem beta? adrenergic receptor proteins.

Conceptor protein of beta? adrenergic receptor gene, and (b) accord alleles of the beta? adrenergic receptor gene, and (b) accord alleles both encode Arg at residue 16 of the beta? adrenergic receptor gene, and (b) accord alleles both encode Arg at residue 16 of the beta? adrenergic receptor gene alleles may be creceptor protein. Beta? adrenergic receptor gene alleles may be creceptor protein. Beta? adrenergic receptor gene alleles may be creceptor protein. Beta? adrenergic receptor gene alleles may be creceptor gene alleles which creceptor gene alleles may be creceptor gene as being linked creceptor gene as general gen
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26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HO
BOUShey H, Chinchilli VM, D
Martin RJ;
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02-OCT-1997.
24-MAR-1997; J00982.
27-MAR-1996; JP-072914.
27-MAR-1996; JP-072914.
(DAIN) DAINIPPON PHARM CO L
(DAIN) K, FURUTANI Y, KAWAShi
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Beta-2 adrenalin receptor
Beta-2 adrenalin subtype;
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amino acid change
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                                                              The probe was a 600 bp fragment of the coding region of the human beta-3 constructed from golya-transmentrative for coding region from adipose tissue cells. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor constructed from polya-RA-Na purified from dop brown adipose tissue cells. Cc constructed from polya-Rayment of the coding region of the human beta-3 croptobe was a 600 bp fragment of the coding region of the human beta-3 cc transmembrane domain 5 (TM5). The full length insert was cloned into M13 cc transmembrane domain 5 (TM5). The full length insert was cloned into M13 cc expressed e.g. in a mammalian cell, by subcloning into an expression expressed e.g. in a mammalian cell, by subcloning into an expression studies, e.g. for differential screening of ligands cc specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

SQ Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
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02-OCT-1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel beta-2 adrenalin receptor sub-type - useful for screening agonists and antagonists and researching asthmatic diseases agonists and antagonists and researching asthmatic diseases claim 5; Page 23-26; 47pp; Japanese.
This sequence encodes the protein of the invention. The protein invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be screening for agonists and antagonists, which are useful in rese
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Drumare MF, Lenzen G, Pietri-Rouxel
WPI; 98-032136/03.
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adrenergic r
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Pred. No. 1.4e
0; Mismatches
Score 77.2; L
Pred. No. 2.2e
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asthmatic diseases

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                                                                                                                                                                                                                                                                                                                                                                                                                                 PT Wild type and mutated sequences of Mycobacterium embCAB operon - PT useful to e.g. identify ethambutol-resistant mycobacterial strains PT and produce antisense sequences to treat mycobacterial infections PS Disclosure; Fig 6A-I; 62pp; English.

CC This is the DNA sequence of the Mycobacterium smegmatis embCAB coperon, which determines resistance to the antimycobacterial drug CC ethambutol (EMB). It includes the embA, embC and embb genes that CC encode proteins (see W73052-54) which are the target of action of CC magmatis for EMB. To identify genes conferring EMB resistance, CC a genomic library from a high level EMB-resistant mutant of M.

CC smegmatis was introduced into wild-type M. smegmatis mc2155. Four CC overlapping cosmids were identified which conferred a resistant CC phenotype. The minimum size fragment capable of conferring EMB CC smegmatis sequence was dequences reverlang 3 homologous open CC resistance was dequences reverlang 3 homologous open CC mycobacteria or to determine the susceptibility of mycobacteria to CC mycobacteria or to determine the susceptibility of mycobacteria to CC EMB. The nucleic acids are also useful in the treatment of mycobacteria infections; anti-DNA or anti-RNA sequences can be CC administered to inhibit embCAB operon mRNA activity (claimed). The CC invention additionally provides for the use of embCAM operon CC cucleic acid sequences as vaccines, or to improve existing
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V45185;
19-OCT-1998 (first
                                atherosclerosis; congestive
                                             Nucleotide sequence encoding human cardiac/brain tolloid-like protein ss; human; cardiac/brain tolloid-like protein; hC/BTLP; restenosis;
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(YESH ) UNIV YESHIVA EINSTEIN COLLEGE
Jacobs WR, Musser J, Telenti A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drug resistance; antibiotic resistance; antimycobacterial;
ethambutol; embCAB operon; infection; vaccine; therapy; ds
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22-JUL-1998.
23-DEC-1997; 310521.
02-JAN-1997; US-0344
                                                                                                                                                                                                                                                                                                                 Hepatitis
Key
cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restenosis, atherosclerosis and congestive heart failure Claim 2; Page 5-10; 34pp; English.
The human cardiacyDrain tolloid-like protein (hC/BTLP) inadequate or excessive activity is associated with restenosis, atherosclerosis, congestive heart failure, chronic obstructive pulmonary disease, benign prostatic hypertrophy, glomerulonephritis, nephritis, fibrosis, gliosis, cirrhosis and anomalous wound healing (e.g. keloids). Disease or susceptibility to disease related to expression or activity of hC/BTLP can be diagnosed by detecting a mutation in the gene encoding hC/BTLP. Polypeptides and polynucleotides of hC/BTLP can be diseases.
                                                                                  misc_difference
                                                                                                                                                                           misc_difference
                                                                                                                                                                                                                                                                                                                         Hepatitis GB virus isolate C large open reading frame. Hepatitis GB virus; HGBV; diagnosis; vaccine; ss. Hepatitis GB virus isolate C genotype 1. Hepatitis GB virus isolate C genotype 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding human cardiac/brain tolloid-like and related products, used for treating and diagnosing, e.g restenosis, atherosclerosis and congestive heart failure
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(SMIK ) SMITHKLINE BEECHAM
Arleth AJ, Elshourbagy NA,
WPI; 98-379062/33.
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                         /note- *base 569 is superfluous to sequence and should be deleted to maintain the reading frame for the
                                                                                                                     /note= "base 494 is sequence and should had maintain the reading
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                                                                                                                                                                                                                   /note= "bases 356-357 are superfluous
coding sequence and should be deleted
maintain the reading frame for the
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RESULT
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Matches 47
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11-DEC-1996.
07-JUN-1996: 109206.
07-JUN-1995: US-480995.
19-APR-1996: US-629463.
(ABBO ) ABBOTT LAB.
CAIRICK RJ. Dawson GJ. Des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic use and vaccine prodn.

Example 1; Page 57-62; 105pp; English.

A previously described large open reading frame (T45828) for A previously described large open reading frame (T45828) for hepatitis GB virus (HGBV) isolate C genotype 1 is provided. The availability of HGBV nucleic acid sequences (see also T45836) obtd.

e.g. by PCR amplification, permits the construction of expression vectors encoding antigenically active regions of the HGBV protein (see also W06536). Novel recombinant HGBV polypeptides are useful as immunoassay reagents for HGBV antigens or antibodies. They can also be used in vaccine prodn., to determine clearance of HGBV from an infected patient and to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1998 (first entry)
23-FEB-1998 (first entry)
Fragment of HGBV NS3 genomic region.
Frimer; hepatitis GB virus; HGBV; serotype; hybridisation; RT-PCR; LCR; reverse transcriptase; probe; amplification; gap ligase chain reaction; blood; organ; detection; diagnosis; ss.
        Oligo.nucleotide(s) specific for hepatitis GB virus-C, useful as probes and primers - for diagnosis, screening blood etc. and design of specific poly; peptide(s)

Example 1; Page 51-56; 96pp; English.

The invention relates to nucleic acid sequences derived from a novel Hepatitis GB virus (HGBV), a form of non-A to-non-E hepatitis, especially the C serotype of the virus. This sequence represents the NS3 region of the virus genome. The probe (corresponding to bases 4245-4432) can be used to detect, by hybridisation, the presence of HGBV-C serotype nucleic acids in a sample following by RT-PCR amplification of the viral genome.
                                                                                                                                                                                Erker JC, Leary TP, Muerhoff AS, WPI; 97-179430/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1092 GCTCCAGCAGGAGGAGGG
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Sequence 9126 BP; 1611 A; 2514 C; 2913
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Birkenmeyer L, Chalmers M,
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14-AUG-1996; U13171.
21-DEC-1995; US-580038.
14-AUG-1995; US-002265.
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primers T96445-6.
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 Oligonucleotides
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Pred. No. 5.
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N. Surowy
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RESULT 1 V10355/c

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V10355 standard; V10355;

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                                                                                                                                                                                                                                                                                                                                                                                                                                         petection of hepatitis GB virus - by reacting test samples with patting and further reaction with second antibody or anti-HGBV antibody and further reaction with second antibody or primers for amplifying viral RNA Example 1; Page 44-50; 62pp; English.

For the E2 antigen (see W63611) of hepatitis GB virus isolate C (HGBV-C). The invention relates to E2 antigenic epitopes (see W63612-16) and methods for detection of HGBV are utilised to E3 samples. Antibodies to the E2 region of HGBV are utilised to capture antigen capture to the E2 region of HGBV are utilised to the propagation, identification, detection and products can be used for and antigen capture PCR. The methods and products can be used for the propagation, identification, detection and isolation of HGBV.

They will also allow the preparation of diagnostics and vaccines for the possible different strains of HGBV, and will have utility
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09-JUL-1998.
23-DEC-1997; U23767.
31-DEC-1996; US-778377.
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V39074 standard; DNA; 9126
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                                                                                                                    1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1998 (first entry)
Hepatitis GB virus E2 gene regi
HGBV; E2 antigen; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB.
Dawson GJ, Dille BJ, Gutierrez RA, Mushahwar IK;
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                                                                                                                                                                                                                                                                                                                                                                                         in screening procedures for anti-viral agents. sequence 9126 BP; 1612 A; 2514 C; 2913
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GCTCCAGCAGGAGGAGGG 1075
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47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT DNA molecule purified from embryo fibroblasts - useful in, e.g. Thibiting wound healing abnormalities and treating fibrosis Claim 4; Pages 30-34; 49pp; English.

CC The present sequence is of a human tolloid-like (mTll) cDNA. This CC sequence was derived from clones isolated from a human placenta genomic CC library. The human Tll gene maps to the 4925-4qter region on chromosome CC 4. As the human Tll gene maps to the 4925-dqter region on chromosome CC protein (mTl), it is expected to be a protease having a key role in CC development and homeostatic processes such as wound healing. The CC invention claims that human Tll protein can be used for promoting CC maturation of extracellular matrix precursors into macromolecular CC structures, for activating growth factors in vivo and in vitro and for accelerating developmental and homeostatic processes when administered CC to a tissue. Human Tll protein may also be used to develop inhibitors CC against lite enzymatic activity. Such inhibitors would be useful in CC preventing fibrosis and excess scarring or other abnormalities of wound CC healing. Specific antibodies raised against the C-terminal region of CC human Tll (W40226) can be used in assays for visualising the production and localisation of mTll protein in cells and tissues.

Sequence 3919 BP; 1089 A; 871 C; 1001 G; 958 T;
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Best Local !
16-FEB-1999.
25-JUL-1997; JP-200625.
25-JUL-1997; JP-200625.
(TOFU) TONEN CORP.
(MPI; 99-197820/17.
P-ESDB; W98969, W98970, W98971, W98972, W98973, W98974, W98975,
W989696, W98977, W98978.
New encoding an aromatic cpd. oxidative decompsn. enzyme - useful the fields of petroleum purification, chemical and drug industries claim 1; Page 7-19; J5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tolloid-like (TII) cDNA Mammallan tolloid-like; mTII; wound healing; fibrosis; growt Homo Bapiens.
                                                                                                                                                                                                      Alcaligenes sp.
J11042088-A.
                                                                                                                                                                                                                                                           10-MAY-1999 (first entry)
Alcaligenes sp. Pox proteins R, A, B, C, D, E, F, G, H and I coding DNA Alcaligenes; PoxE; PoxE; PoxB; PoxB; PoxB; PoxH; PoxI; aromatic; oxidative; petroleum purification; chemical industry; PoxI; aromatic; oxidative; petroleum purification; chemical industry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES FOUND. Greenspan DS, Hoffman GG, Takahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9745528-A2.
04-DEC-1997.
30-MAY-1997; U09078.
30-MAY-1996; US-018684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 GCGGTCCGCGCTGATGTGCGGGGCTAGGGGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 aagggacgaggtgtggtggtgggcattgggcattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 cagcgccttcttgctggcacccaatagaagccattgcgccggaccacgacgtcacgcagca 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACCCCATCCTCCTCCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosis; growth factor; extracellular matrix; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 648. .3689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human mTll protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                             ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27.8; D
Pred. No. 7.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3919;
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                                                                                                                                                                                      That encoding BssHII restriction and methylase enzymes - useful for molecular cloning and recombinant production of the enzymes Example 1; Fig 1A-B; Spp; English.

C This cDNA encodes a Bacillus stearothermophilus BssHII multi-specific methylase enzyme. The specification provides sequences of BssHII centonic endonuclease gene (bssHIIM) and bssHIII restriction endonuclease gene (bssHIIM). A recombinant vector containing these genes are used to transform host cells to recombinantly produce the BssHII restriction enzyme (BssHIIR), and its cognate methylase enzyme (BssHIIM), for use in genetic engineering. The enzymes recognise the sequence 5'GCGCGC3', and the methylase also recognises the sequences 5'RCGCGC3', and the methylase also recognises the sequences 5'RCGCGC3', and the methylase also recognises the sequences 5'RCGCGC3', and the methylase also recognises the sequences 1608 BP; 390 A; 440 C; 489 G; 289 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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Best Local
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V43679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multi-specific BssHII methylase enzyme (BssHIIM1) encoding cDNA. Methylase; restriction endonuclease; Bacillus stearothermophilus; enzyme; multi-specific; genetic engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9770
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Sequence 12019 BP; 2015 A; 4104 C; 4151 G; 1747 T;
                                                                                                                                                                                                                                                                                                                                                                                                                     X1ao J, Xu S;
WPI; 98-436530/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5786195-A.
28-JUL-1998.
12-MAR-1997; 815688.
12-MAR-1997; US-815688.
(NEWE ) NEW ENGLAND BIOLABS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus stearothermophilus.
Key Location/Qua
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                                                          449
509 TCATCGTGGGCATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                     80 gggtggtgggcatgggc 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCACGCTGTGATGGTCGTGCTCGTCCCAGGCCT 9736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCATCGCTGTCGACGCGGAAGCCCATGTAGTCCATGCCCGGGCTGTCGGCCTCGCGCAG 9771
                                                                         TGTCATGGAAACTCATCAACGCATGGGACTACGGAGTGGCGCAGAAGAGGGGAGCGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                    1 Similarity
46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                25.8%;
59.7%;
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525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Multi-specific BssHII methylase enzyme (BssHIIM1)"
                                                                                                                  Score 27.4; DB Pred. No. 9.1; O; Mismatches
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Pred.
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No. 8
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                                                                                                                                              Length 1608;
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RESULT

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PS Claim 1; Page 988; 2245pp; Japanese.
Cd obble-stranded DNA (or its complementary strand or the corresp.
Cd obble-stranded DNA) which comprises one of the 7837 "GS" sequences
Cd 91ven in T19001-T26837 and which is able to hybridise to part of
Cd 91ven in T19001-T26837 and which is claimed. The GS (Gene Signature)
CC human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC grom various human tissues; synthesis of cDNA was initiated from the
CC untranslated sequence is unique to a particular mRNA species, almost
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC determined (esp. using primers and probes derived from the GS
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC crecognising different cell types.
CC Sequences 323 BP; 111 A; 47 C; 63 G; 95 T;
THOSUEN
THOSUE
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
W09514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature;
human; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene signature HUMGS03413
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                                                           26-DEC-1995.
12-JUN-1990; US-537183.
12-JUN-1990; US-537183.
12-AUG-1993; US-103739.
02-AUG-1993; US-103739.
28-CCT-1994; WO-U12444.
(PION-) PIONEER HI-BRED ALBORNE, Beach LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-206931/27.
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12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                         10-JUL-1996 (first entry)
Nucleotide sequence for mediating male fertility in plants.
Male fertility; plant; microsporogenesis; tassel development;
maize; sterile; fertile; transformed plant; female parent;
hybrid seed; ds.
                                                                                                                                                                                                                                                              Zea mays.
US5478369-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T10928 standard;
      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tggcacccaatagaagccatgcgccggaccacgacgtcacgcagcaaagggacgaggtgt 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTGGTCGTCA 104
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                                     96-057646/06.
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44; Conservative
      R88502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 1419
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61.1%;
                                                                                                   INT INC
                                                                       Howard J,
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Pred. No. 8.6;
0; Mismatches
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detection;
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                                                                                                                                                                                                                                                                                                                                                                                                       MS45;
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SCC CCC CCC PPT PTT
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V62709
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Best Local S
Matches 38
Search completed: September Job time: 4090 sec
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                                                                                                     8
                                                                                                                                   Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a nucleic acid sequence which mediates male fertility in plants. This sequence encodes an amino acid sequence which is responsible for one of the steps in microsporogenesis, which is responsible for one of the steps in microsporogenesis, specifically tassel development. This cDNA was isolated from a specifically tassel development. This cDNA is considered this tassel derived cDNA and was named MS45. The introduction of this tassel derived cDNA into a plant, pref. maize, which is normally male sterile causes it to be fertile. Such transformed plants may be used as female parents in the production of hybrid seeds. Sequence 1419 BP; 304 A; 387 C; 473 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                         US5824524-A.
20-OCT-1998.
07-JUN-1995; 474404.
02-AUG-1993; US-103739.
12-JUN-1990; US-537183.
07-JUN-1995; US-474404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding a protein critical for male fertility plants - used to produce plants, esp. maize, that are norma sterile but can be induced to fertility, esp. for use in hyb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prodn
Claim 4; Column 25-27; 27pp; English
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V62709;
24-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143 CGAGGACCGGGGCCACGAGGTGATGAAGCTGGTGAGCGAGGTGCGGGAGGTGGGCA 1198
                                                                                                                                                                                                                                           fertility gene fertility gene MS45 can be repressed as a method for Claim 2; Column 37-40; 40pp; English.

The maize male fertility gene MS45 can be repressed as a method for The maize male fertility in a plant. This method can be used especially mediating male fertility in a plant. The endogenous gene can be inactivated.

The modern of the maize seed. The endogenous gene can be inactivated as a method for the mediating male fertility in a plant. The endogenous gene can be inactivated as a method for the maize seed.
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Albertsen MC, Beach LR, Howard J, Hu
WPI; 98-582558/49.
P-PSDB; W77413.
Production of male-sterile plants -
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Sequence
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                                                                                                                                                                                                             producing hybrid maize seed. The endogenous gene the control of an inducible promoter can be used ivate the gene when fertile plants are desired. uence 1419 BP; 304 A; 387 C; 473 G;
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38; Conser
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/note= "No
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Pred. No. 10;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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PCT-US91-00909-1
US-08-822-586-46
US-08-991-408-1
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PCT-US91-00909-3
; Sequence 3, Applicati;
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US91/0
FILING DATE: 19910208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 91000
REFERENCE/DOCKET NUMBER: 99000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPAX: 206-622-4900
TELEPAX: 3723836
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: United States
ZIT: 98104-7992
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   MOLECULE TYPE: FEATURE:
                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
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100.0%; ilarity 100.0%; Conservative 0
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US-08-458-819-7
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US-08-933-962-5
PCT-US94-05365-5
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                  Score 106; DB 6;
Pred. No. 4.6e-24;
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Minimum Maximum

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Sequence: Title: Perfect score: OM nucleic -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00909
FILING DATE: 19910208
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 000008 10800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application:
Sequence 46, Application US/08822586 Patent No. 6015890
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Best Local S
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1254 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                61 cagcaaagggacgaggtgtgggtggtgggc 90
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206-60
TELEX: 3723836
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 CITY: Seattle
                                                                                                  76 GAGGAACGGACGAAGCATGGGTGGTAGGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sledziewski, Andrzej Z.
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                              57.7%;
80.0%;
                                                                                                                                                                                                                                Score 61.2; DB 6; Length 1254; Pred. No. 1.9e-10; 0; Mismatches 18; Indels 0
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; MOLECULE TYPE: Ge
; HYPOTHETICAL: NO
US-08-822-586-46
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US-08-991-408-1/c
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APPLICANT: WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT: AMALIO TELERTI

TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND TITLE OF INVENTION: MUTANTS THEREOF NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
AMDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATII
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                         APPLICANT: ARLETH, ANTHOAPPLICANT: WILLETTE, ROI APPLICANT: ELSHOURBAGY, APPLICANT: LI, XIAOTONG
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                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                   TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE TITLE OF INVENTION: PROTEIN
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                        62 agcaaagggacgaggtgtgggtggtggcatgggcatcgtcatg 105
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TOPOLOGY: linear
                                                STREET: P.O. BUX >0 CITY: VALLEY FORGE
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COUNTRY: USA
ZIP: 19482
                                      STATE:
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                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                    ARLETH, ANTHONY J.
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                                                                          RATNER & PRESTIA O. BOX 980
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58.7%;
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COMPUTER READABLE FORM:

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Best Local s
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GENERAL IN
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REFERENCE/DOCKET NUMBER: ATG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
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SEQUENCE CHARACTERISTICS:
LENGTH: 5145 base pairs
TYPE: nucleic acid
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                  TITLE OF INVENTION: Detection of Hepatitis GB Virus
TITLE OF INVENTION: Genotypes
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 60/0
FILING DATE: 02-JAN-1997
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                                                                                                                                   STREET: 100 Abbott
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 aagggacgaggtgtgggtggtgggcatgggcatcg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/991,408
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                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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APPLICATION DATA:
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                                                                                                                                                                                                                                                 Erker, J. C.
Dosal, S. M
Mushahwar, I.
Chalmers, M.
Dawson, G. J.
                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                               Birkenmeyer, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                  Simons,
                                                                                                                                                                                                                                                                                                                                                                                 Muerhoff, A. S.
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             Version #1.30
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                                                TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1152 CGGGCGCCCTTGTGACATGCCCGCCATAGTGACCAGGAGGAGGAGGAGACCATGACAATACGCT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1092 GCTCCAGCAGGAGGAGGG 1075
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: POTENDSKI, PTISCILLA E.
REGISTRATION UNMBER: 33,207
REFERENCE/DOCKET NUMBER: 5793
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Simons, J. N. APPLICANT: Desai, S. M. APPLICANT: Mushahwar, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 26.8%;
Local Similarity 60.3%;
les 47; Conservative
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REFERENCE/DOCKET NUMBER: 5793.US.01
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STRANDEDNESS:
                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Abbott Park
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                                     9126 base pairs
                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                              US/08/639,857
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                                                                                                                                                  5793.US.P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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; MOLECULE TYPE: US-08-639-857-3
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                                                                                                                                                                                                                                                                        ; LOCATION: 648..368
; OTHER INFORMATION:
US-08-866-650-4
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Best Local Similarity
Matches 47; Conserv
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Patent No. 5939321
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                                                                                                                      Matches 53;
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 608-251-9100 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1152 CGGGCGCGCCTTGTGACATGCCCGCCATAGTGACCAGGAGGAAGACCATGACAATACGCT 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
APPLICANT: HOFFman, Daniel S
APPLICANT: HOFFman, Guy G
APPLICANT: HOFFman, G
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELECPHONE: 608-251-5000
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ORIGINAL SOURCE:
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656 CAACCCCATCCTCCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1 South Pinckney Street
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LOCATION: 648..3689
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                                                                                                                                                                                                                                                                                                            /product= "human mTll protein"
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Pred. No. 2.
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Pred. No. 3.3;
0; Mismatches
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Mismatches
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US-09-021-287-4/c
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RESULT 9
US-08-815-688A-2
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 53703
                                                                                                                 656 CAACCCCATCCTCCTCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
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STREET: 1 South Pinckney Street
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                                                         596 GCGGTCCGCGCTGATGTGCGGGGCTAGGGGCACCG 562
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                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                                                                                                            Local Similarity
les 53; Conserv
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                                                                                  66 aagggacgaggtgtgggtggtgggcatgggcatcg 100
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                                                                                                                                       cagcgccttcttgctggcacccaatagaagccatgcggcgggaccacgacgtcacgcagca 65
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                                                                                                                                                                                                                                                                                                                                                                                                                3919 base pairs
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55.8%;
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Pred. No. 3.
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                                                                                                                          RESULT 10
US-08-103-739B-1
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                                                                                           Sequence 1, Application US/08103739B Patent No. 5478369
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   Matches
                                                              GENERAL INFORMATION:
APPLICANT: ALBERT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,688A
FILING DATE: 12-MAR-1997
                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: WILLIAMS, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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TITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: X1ao,
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                   PPLICANT:
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                                                                                                                                                                                                        80 gggtggtgggcatgggc 96
                                                                                                                                                                                                                                                                          20 tggcacccaatagaagccatgcgccggaccacgacgtcacgcaggcaaagggacgaggtgt 79
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OTHER INFORMATION:
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REGISTRATION NUMBER: 3090
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                   Conservative
                                             BEACH, Larry R.
                                                              ALBERTSEN, Marc C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu, Shuang-yong
                                HOWARD,
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59.7%;
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DNA Sequences Mediating Male Fertility
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Pred. No. 3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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APPLICANT: ALBERT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,404
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1143 CGAGGACCGGGGCCACGAGGTGATGAAGCTGGTGAGCGAGGTGCGGGAGGTGGGCA 1198
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APPLICATION NUMBER: US 07
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleotide Sequences Mediating NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 02-AUG-1993
CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                             CITY: Des Moines
                                                                                                                                                                                                            STREET:
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67.9%;
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Pred. No. 4
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APPLICATION NUMBER:

02-AUG-1993

US 08/103,739

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; MOLECULE TYPE: CDNA US-08-474-404-1
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Best Local :
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TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
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REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0125R2R3
TELECOMMUNICATION INFORMATION:
                                                                                                         APPLICATION NUMBER: US 08
FILING DATE: 02-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
DETTION DESCRIPTION DESCRIPTION
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TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOWARD, John A.
APPLICANT: HUFFMAN, Gary A.
TITLE OF INVENTION: Nucleotide Sequences Mediating Fertility and Method of Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248 4897
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les 38; Conserv
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ucleic acid
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700 Capital Square, 400 Locust Street
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Pred. No. 4
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1143 CGAGGACCGGGGCCACGAGGTGATGAAGCTGGTGAGCGAGGTGCGGAGGTGGGCA 1198

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MOLECULE TYPE:
US-08-485-845-1
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Best Local 9
                                                   Query Match
Best Local Similarity
                                       Matches
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 0
FILING DATE: 12-UN-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 02-AUG-
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MEDIUM TYPE: Floppy
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STRANDEDNESS: doubl
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Des Moines
STATE: Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OFILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                    NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,7
36 ccatgcgccggaccacgacgtcacgcagcaaagggacgaggtgtggggtggtgggca 91
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milarity 67.9%;
Conservative
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VENTION: Nucleotide Sequences Mediating Fertility and Method of Usin
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                                       Conservative
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248-1:
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Pred. No. 4.
                                                      Score 27.2; D
Pred. No. 4.3;
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US-08-648-657-14

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RESULT 15
PCT-US95-14418-3
Sequence 3, Application PC/TUS9514418
GENERAL INFORMATION:
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US-08-648-657-14
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GENERAL INFORMATION:
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Best Local
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 219/

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1000

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TITLE OF INVENTION: THERMOSTABLE
TITLE OF INVENTION: POLYMERASES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                      1426 ATGGCCTTCAACATG 1440
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OPERATING SYSTEM: IBM P.C.
SOPTWARE: WORD PORFECT 5.1
CURRENT APPLICATION DATA:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION UMBER: US 08/455,686
FILING DATE: May 31, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davis, Maria APPLICANT: Moffett, R. Bruce APPLICANT: Fuller, Carl W.
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 633 West Fit
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Similarity 60.0%;
45; Conservative
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633 West Fifth Street
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Pred. No. 5;
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Search completed: September 12, Job time: 3935 sec
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NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1794 base pairs
                                                                                                                                       1474
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                           1534 ATGGCCTTCAACATG 1548
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CITY: Chicago
STATE: Illinoi
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6300 Sears Tower, 233 South Wacker Drive
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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and is derived by analysis of the total score distribution.
C18250 377 bp mRNA EST UZ-UCI-1390 C18250 Human placenta cDNA (TFUjiwara) Homo sapiens cDNA clone GEN-559E06 5', mRNA sequence.
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AA661315 va15507.x
AA470234 vd90h08.r
AA470234 vd90h08.r
AA254331 va15508.r
AV129211 AV129211
AV298968 AV298968
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AV107772 AV107772
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AV302729 AV302729
AA980400 ua52g10.r
AL135598 DKRYZP762E
AV323541 AV323541
AA980836 ua46c02.r
A1021469 ub08f07.r
AA616441 vo09504.r
AM185521 se80h01.y
AA458282 vg48all.r
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A1838527 UI-M-ALO-
AA607055 vm95e04.r
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AV352055 AV352055
AV138058 AV138058
AW225456 SWYD25CAU
AQ858041 nbeb0011N
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AU063749 AU063749
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AA278503 zs81e04.r
A1706391 UI-R-AE1-
C29133 C29133 Rice
AA218070 mv01q03.r
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C18250.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiwara, T., Hirano, H., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y., Kyushiki, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T., Maekawa, H., Nakamura, Y. and Takahashi, E.
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Unpublished (1996)
Contact: Tsutomu Fuj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 377)
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98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA980445 744 bp mkNA ua41602.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone ua41602.rl Soares_mammary_gland_NbMMG Musculus cDNA clone ua41602.rl Soares_mammary_gland_NbMMG Musculus clone ua41602.rl Soares_mammary_gland_NbMG Musculus clone ua41602.r
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                                                                                   The Washu-HHMI Mouse EST Project
Unpublished (1996)
On Apr 7, 1998 this sequence version repla
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                           Mammaiia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; 1 (bases 1 to 744)
1 (bases 1 to 744)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc Marra, M., Hillier, L., Allen, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMAN);, mRNA sequence.
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                                         Tel: 314 286 1800
Fax: 314 286 1810
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                      mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="GEN-559E06"
/clone="Muman placenta cDNA (TFujiwara)"
/tissue_type="placenta"
/tissue_type="placenta"
/tissue_type="placenta"
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90.7%;
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Primates;
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AV306064/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 21 (bases 1 to 165)

E 1 (bases 1 to 165)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadoca, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watehiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGAACGGGACGAAGCGTGGGGTTGTGGGCATGGCAATCCTCATGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV306064 RIKEN full-length enriched, 8 days cona clone 5730534007 3', mRNA sequence.
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1 219 c 213 g 155 t
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/dev_stage="4 weeks"
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/clone-"IMAGE:1349283"
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/strain="C57BL/6J"
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84.9%;
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No. 5.3e-14;
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RESULT 4
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                                                                                                                                        40 GGAATTGGGGAAAGTGTAGT 21
                                                                                                                                                                                                                     CCATGGAAGCCAGGTGCCAGACCCCCAAGGGAAGCAGCCCCGGTCGGGGGGTGGGGGTGGG 41
                                                                                                                                                                    gggcatgggcatcgtcatgt 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Aklyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           AA209561 255 bp mRNA mu71h05.r1 Soares mouse lymph node NbMLN IMAGE:6444889 5', mRNA sequence.
AA209561 AA209561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013 Fax: +81-298-36-9098
AA209561.1 GI:1807898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched, 8 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B"
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                                                                                                                                                                                                                                                                                31.7%;
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                                              Mus
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                                              musculus cDNA clone
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                                                                                                                                                                                                                                                                      gggcatgggcatcgtc 102
                                                                                                                                                                                                                                                                                                                                CCATGGAGGCCAGGTGCCAGACCCCCAAGGGAAGCAGCCCCGGTCGGGGGGTGGGGTGGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
Contact: Warra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 255)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                               A1661315 286 bp mRNA FWA15677.x1 Soares mouse lymph node NbMLN IMAGE:723013 3', mRNA sequence.
A1661315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Mus musculus
                                        EST
                                                           AI661315.1 GI:4764898
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house mouse.
                     house mouse.
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h quality sequence stop: 246.
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

68 c 72 g 54 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
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/dev_stage="4 weeks"
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/clone="IMAGE:644889"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%;
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Pred. No. 4.2;
0; Mismatches
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Mus musculus
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                                                                                                                         cDNA clone
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                              gggcatgggcatcgtc 102
                                                                                                                                                                                                                                                                                                                                                                               CCATGGAGGCCAGGTGCCAGACCCCCAAGGGAAGCCACCCCGGTCGGGGGGTGGGGGTGGG 127
                                                                                                                                                                                                                                                                                              GGAGTGGGGCAAGGTC 143
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3247027.
Other_ESTs: va15f07.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                        Mus musculus
                                                                                                                                                                  vd90h08.rl Soares
                                                                                                                                                                                         AA470234
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                        AA470234.1 GI:2197543
                                                                                                                         AA470234
                                                                                                                                            5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       data is from the 3' end
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This clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                house mouse.
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:723013"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Pred. No. 4.2;
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RESULT 7
AV055159/c
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nes 49; Conser
Mus musculus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                                                                                                                AV055159
AV055159
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On Jan 19, 1998 this sequence version replaced gi:2151946.
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                          AV055159
AV055159.1
                                                                                                                  AV055159 Mus musculus pancreas C57BL/6J adult Mus musculus clone 1810034A24, mRNA sequence.
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                                                          house mouse
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/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
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a 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:807903"
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                                                                                          GI:5154906
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               Chordata; Craniata; Vertebrata; Eutéleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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               JOURNAL
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Best Local
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COMMENT
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On Apr 3C, 1999 this sequence version replaced g1:5866824.
Contact: Chie Owa
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 23)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                    AA254331 233 bp mRNA val5f08.rl Soares mouse lymph node IMAGE:723015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Projec
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AA254331.1 GI:1888943
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                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pancreas"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="1810034A24"
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Carrinci.P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawal,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H. Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yanamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. RIKEN Mouse ESTs
Unpublished (1999)
On Aug 21, 1998 this sequence version replaced gi:3707190.
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                  AV129211 178 bp mRNA EST AV129211 Mus musculus C57BL/6J 11-day embryo Mus clone 2700066J24, mRNA sequence.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musidaes; 1 to 178)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo." 73 c 65 g 52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:723015"
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/dev_stage="4 weeks"
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                                                                                                                                                                                             RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, S., Fukuda, S., Tukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shibata, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shibata, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Yoshino, M., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Nothide, M., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Riken, Mouse ESTS (Konno, H., et al.)

On Oct 30, 1998 this sequence version replaced gi:3816340.
On Oct 30, 1998 this sequence version replaced gi:3816340.
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of full length cDNA
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(7):524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                             The Institute of Physical and Chemical Research (RIKEN), Genomic
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/strain="C57BL/6J"
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/clone="2700066J24"
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50 c 47 g 43 t
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                                                                                                       AV297381 243 bp mRNA EST
AV297381 RIKEN full-length enriched, 8 days
cDNA clone 5730448106 3', mRNA sequence.
AV297381 GI:6329460
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Corninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okazaki,Y
                                                                     house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="8 days embryo"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730463007"
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Query Match Best Local Similarity "hes 48; Conserve

Conservative

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29.4%;

Score 31.2; Di Pred. No. 12; 0; Mismatches

BG 60; 28;

Length Indels

243; 0

Gaps

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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukunda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Saito, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Wattahiki, A., Wathanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Woshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al.)

On Jun 15, 1998 this sequence version replaced gi:3224201.
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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                         57
              details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730448I06"
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/lab_host="DH10B"
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Mammalia; Eutheria;
1 (bases 1 to 187)
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AV107772.1 GI:5255320
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Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@rtc.riken.go.jp
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes k
Thermostabilization and thermoactivation for the synthesis of full length cDN
trehalose and its application for the synthesis of full length cDN
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
(Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
please visit our web site (http://genome.rtc.riken.go.jp) for
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Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Science Laboratory
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47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="liver"
/dev_stage="13-day embryo"
/dev_stage="49 g 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="2510040L09"
/clone_lib="Mus musculus liver C57BL/6J 13-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                       27.9%;
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AV340114/c
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RS KONNO, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Kusada, I., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Ishii, Y., Kojima, Y., Koya, S., Kusakabe, M., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Sano, M., Sato, K., Shibata, K., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, K., Shibata, K., Shibata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Suzuki, H., Sano, M., Sato, M., Tominaga, N., Suzuki, H., Suzuki, H., Sano, M., Sato, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Sano, M., Sato, M.
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AV340114 RIKEN full-length enriched, adult male olfactory brain
musculus cDNA clone 6430513A21 3', mRNA sequence.
AV340114 GI:6380166
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) 1toh, M., Kitsunai, T., Aklyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 1044, 1360.
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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Tel: +81-298-36-9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +81-298-36-9098
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                                                                                                                                                             /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory Genomic Sciences Center and Genome Ricence Laboratory Genomic Science Center and Genome Ricence Laboratory Genomic Science Center and Genome Science Laboratory Genomic Science Center and Genome Ricence Laboratory Genomic Science Center and Genome Countries of the Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olfactory brain"
/sex="male"
        contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGCTCTATTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="olfactory brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, adult male
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Yoneda, Y.,

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RESULT 14
A1838527/c
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AUTHORS
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Best Local S
Matches 47
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI838527 305 bp mRNA EST 1.
UI-M-ALO-abp-a-12-0-UI.sl NIH_BMAP_MCO Mus musculus
UI-M-ALO-abp-a-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                     The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized prefrontal cortex library CDNA Library Preparation:

M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Feb 24, 1999 this sequence version replaced gi:4061710. Contact: Chin, H
Contact: Thin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus 1 (bases 1 to 305)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI838527
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                               ord will be updated accordingly when that means is determined primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
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/lab_host="DH108 (Life Technologies)"
                                                                                                                                                                         Location/Qualifiers
                                                                                                                               /organism="Mus musculus"
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Pred. No. 36;
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On Jan 14, 1998 this sequence version replaced g1:1877600.
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA607055 354 bp mRNA EST vm95e04.r1 Knowles Solter mouse blastocyst Bl Mus clone IMAGE:1006014 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 354)
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3 c 81 g 78 t
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. primer: Sali(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were
                                                                                      /strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="Taxon:10090"
/clone="Ib="Knowles Solter mouse blastocyst
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
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cloned into the NotI/SalI sites of a pSPORT vector (Life

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Technologies). Two different size selections: B1 (larger inserts) and B3."

BASE COUNT 78 a 95 c 101 g 80 t

ORIGIN

Query Match 27.9%; Score 29.6; DB 28; Length 354;
Best Local Similarity 61.8%; Pred. No. 37;
Best Local Similarity 61.8%; P
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: gb_bal: *

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3: gb_om: *

4: gb_ph: *

6: gb_ph: *

6: gb_ph: *

9: gb_pr: *

9: gb_pr: *

11: gb_or: *

12: gb_or: *

13: gb_or: *

14: gb_ln: *

15: em_hum1: *

16: em_hum2: *

9: em_li: *

9: em_li: *

9: em_li: *

9: em_br: *

10: em_or: *

11: em_or: *

11: em_br: *

12: em_br: *

13: em_br: *

14: em_br: *

15: em_br: *

16: em_br: *

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18: em_br: *

19: em_br: *

19: em_br: *

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11: em_br: *

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12: gb_htg1: *

13: gb_htg1: *

14: gb_htg3: *

15: em_brig5: *

16: em_brig5: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Green, S.A., Turki, J., Innis, M. and Liggett, S.B. adrenergic Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
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/db_xref="taxon:9606"
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the beta 2-adrenergic
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U95094 Xenopus lae
X15643 Mouse gene
AF000134 Sus scrof
AE000106 Rhizobium
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/gene="ADRB2" /codon_start=1

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Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor properties of the receptor J. 1910. Chem. 268 (31), 23116-23121 (1993)
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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Liggett, S.B. and Green, S.A.
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Blochemistry 33 (32), 9414-9419 (1994)
                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1242)
2 (bases 1 to 1242)
2 (creen.S.A., Cole,G., Jacinto,M., Innis,M. and Liggett,S.B.
A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor
J. Biol. Chem. 268 (31), 23116-23121 (1993)
                                                                                                                                 Submitted (04-SEP-1997) Medicine, Univ of Submitted (04-SEP-1997) Medicine, Univ of Ave ML670564, Cincinnati, OH 45267-0564,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       Erratum:[[published erratum appears in Biochemistry 1994 Nov 29:33(47):14368]]
4 (bases 1 to 1242)
                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 94043092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects pan. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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                                                                                                               ML670564, Cincinnati, OH Location/Qualifiers
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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LAIVFGNVLVITAKEERLQTVTNYFITSLACADLVMGLAVVBGAAHILMKMMTFG
NEWCEEWTSIDVLCVTASIETLCVTAVDRYFATTSPFKYGSLLTKNKARVILLMVNU
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/protein_id="AABB2150.1"
/db_xref="GI:2570531"
/gene="ADRB2"
1..1242
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/note="Val34 to Met polymorphism"
                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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19; Conser
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Location/Qualifiers
1. .1286
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Eutheria; Primates; Catarrhini;
1 (bases 1 to 1286)
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ILMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLMWIGYVNSGENPLIYCRSPDFRI
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/chromosome="5"
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                                                                                                                                                                                                                                                                        'note="
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Rupert, J.R. and Hochachka, P.W.
Direct Submission
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Rupert,J.R. and Hochachka,P.W.
Beta-2-adrenergic receptor allele frequencies in two native
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LAIVEGNVLVITAIAKFERLQTVTNYEITSLACADLVMGLAVVPFGAAHILMKMWTFG
NEWCEEWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
SGLXSELPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                        /replace="C/T"
349 c 3
                                                                                                                                                                                                                                                                                                                                                                                      AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEYYILLNWIGYVNSGFNPLIYCRSDDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="beta-2-adrenergic receptor"
/protein_id="AAD48036.1"
/db_xref="GI:5714688"
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Macaca mulatta beta-2 adrenergic receptor (B2AR) mRNA, complete
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Rupert, J.L. and Hochachka, P.W.
Beta 2 adrenergic receptor allele frequencies in two
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beta-2 adrenergle receptor.
Macaca mulatta cDNA to mRNA.
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Amend, A.M. and Guan, X.M.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                       Macaca mulatta
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Rupert, J.L. and Hochachka, P.W.
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/protein_id-"AAF20199.1"
/protein_id-"AAF20199.1"
/db_xref-"Gi:66546496"
/translation-"MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
/translation-"MGQPGNGSAFLLAPNGSHAPDHDVLVTQAVDEVGAVHILMKWNTEG
LAIVEGNVLVITAIAKERELCJTVTNVETITSLACADLVMCLAVVEFGAAHILMKWNTEG
NEWCEFWTSIDVLCVTASIETLCVIAVDRYFALTISPEKVGSLITKNKARVIILMKWNTEG
NEWCEFWTSIDVLCVTASIETLCVIAVDRYFALTISPEKVGSLITKNKARVIILMKWNTY
SGLTSFLDIQHHWYRATHQEAINCYANETCCDDFTNQAYAIASSIVSFYVDLVIMVFV
YSRVFDEAKROLQKIDKSEGRRHVQNLSQVEDDGRTGHGLRRSSKFCLKEHKALKTLG
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/sex="female"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGGCAGCGCCTTCTTGC
                                           Direct Submission
Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases
substantial corrections are reported in [2]
Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1970)
Chung, F. Z., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors
FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloning, sequencing, and expression of the rhesus monkey beta adrenergic receptor DNA Cell Biol. 14 (9), 753-757 (1995) 95398843
                                                                                                                          2 (bases 1 to 1970)
Kerlavage, A.R.
                                                                                                                                                                                                                                                                                                                                                                                  beta-adrenergic receptor.
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X04827.1 GI:29372
                                                                                                                                                                87105974
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LAIVFGNYLVITAIAKEERLQYTYNYEITSLACADLVMGLYVPFGAAHILMKMMTFG
NEWCEEWTSIDVLCVTASIETLCVIAVDRYBAITSPFKYGSLLTKNKARDKILLMVMVFV
SGLTSFLPIOMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSFVVPLVIMVFV
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41. .1288
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1289. 1320
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IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSGFNPLIYCRSPDFRI
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/product_"beta-2 adrenergic receptor"
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/db_xref="GI:1004339"
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/db_xref-"taxon:9544"
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/organism="Homo sapiens"
                                  Location/Qualifiers
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1 Similarity 100.0%;
19; Conservation
                                                                                                                                                                       Direct Submission submitted (20-OCT-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 2305)
Schoffeld, P.R., Rhee, L.M. and Peralta, E.G.
                                                                                                                                                                                                         Schofield, P.R.
                                                                                                                                                                                                                                                         Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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gene for beta-adrenergic
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1952. .1957
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1502. ..
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:P07550"
/translation="McQcGNCSAFILAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIV/translation="McQcGNCSAFILAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIVLAIVEGNVLVITAIAKFERLQTVTNYEITSLACADLVMGLAVVPEGAAHILMKMWTFGUFWCEFWTSLDVLCYTASIETICVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIVSGLTSFLPIQMYAIASSIVSFYVPLVIMVFV
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/clone_lib="neonatal human brain stem"
/rote="beta-adrenergic receptor (AA 1-413)"
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1. .2305
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508 c 482 g
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                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Maniatis human"
/clone="lambdahbetaAR17"
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                                /note="beta-adrenergic receptor (AA 1 - 413)"
                 codon_start=1
                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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1 (bases 1 to 3451)

Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Dixon, R.A., Keller, P., Caron, M.G. and Lefkowitz, R.J.

Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
                                                                       cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human beta-2-adrenergic
M15169 J02728 M16106
M15169.1 GI:178201
                                                                                                                                                                      Kobilka, B.K., Dixon, R.A., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Sigal, I.S., Yang-Feng, T.L., Franck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adrenergic receptor.
Homo sapiens (clone: pTF.) (tissue library: Evan
                                                                                                                                                        and Lefkowitz, R.J.
                                                                                                                                                                                                                                                                        regions
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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1007. .:
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LAIVEGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPEGAAHILMKMWTFG
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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1712. 1774
/note-"membrane spanning domain VII"
616 c 649 g 545 t
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/note="membrane spanning domain IV"
1385. .1450
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1114 ..1180
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
Location/Qualifiers
1. .3451
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1616. .1687
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1247. .1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:29371"
/db_xref="SWISS-PROT:P07550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3451 bp
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100.0%; Pred. No.
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                                                           Sci. U.S.A.
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                                                           84 (1), 46-50 (1987)
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HUMADRBRA
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3458)
Emorine, L.J., Marullo, S., Delavier-Klutchko, C., Kaveri, S.V.,
Durieu-Trautmann, O. and Strosberg, A.D.
Structure of the gene for human beta 2-adrenergic receptor:
                                                                                                                                         adrenergic receptor; beta-2 adrenergic receptor. Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis
                                                                                                                                                                           J02960.1 GI:178203
 expression and promoter characterization Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6
                                                                                                                                                                                                       Human beta-2-adrenergic
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                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV LAIVECNVLVITAIAKERLQTVTNYFITSLACADLVMCLAVVEPGAAHLLMKMWTEG NEWCEWTSIDVLCVTASIETLCVIAVDRYFAITSPEKVGSLITKNKARVIILMVWIV SGLTSFLYDIMWYRAVHQEALNCYANETCCDEFTNQAYAIASSIYSFYVPLVIMVFV YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKCHKALKTLG IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLMWIGYVNSGFNPLIYCRSPDERI
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873 c 895 g
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/protein_id="AAA88015.1"
/db_xref="GI:178202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GDB:G00-120-541"
/protein_id="AAA88014.1"
/db_xref="GI:560761"
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1369. .3383
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/db_xref="taxon:9606"
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/note="b-2-adr
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Pred. No.
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KEYWORDS
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Draft entry and computer-readable copy provided by L.J.Emorine, 25-AUG-1987.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
19; Conserv
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132858)
DOE Joint Genome Institute.
                                                                                                                                                                                                            SEQUENCE, 3
AC011354
                                                                                                                                                                                                                                                     ACO11354 132858 bp DNA
Homo sapiens chromosome 5 clone
                                                                                                                      Homo sapiens
                                                                                                                                                          AC011354.1 GI:6013586
HTG; HTGS_PHASE2; HTGS_DRAFT
Sequencing of Human Chromosome
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ATEEPKAPGLACKHTTSSFSPLGPARVAGKQWMPALQGAVGPRPGQPOEKEGEGGRGGK
GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
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890 c 886 g
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/product="beta-2 adrenergic receptor"
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INGTETLCWLPFFIVNIYHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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1264. _2505
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1055. .3057
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/map="5q31-q32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="H-beta-R-[9,10,11]."
/cell_line="A431"
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CIT-HSPC_354F19, WORKING DRAFT
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FEATURES
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submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
www.jgi.doe.gov.

* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contlys
are represented as runs of N. The order of the pleces
are represented as runs of N. The order of the pleces
sis believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 1161: contig of 1161 bp in length
1 162 60531: contig of 59370 bp in length
1 132858: contig of 59370 bp in length
1 132858: contig of 73327 bp in length
1 132858: contig of 73327 bp in length
www.jgi.doe.gov.
* NOTE: This is a 'working draft' sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* I 134419: contig of 134419 bp in length.
* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACULI334 134419 bp DNA HTG
Homo sapiens chromosome 5 clone CIT-HSPC_235N17,
SEQUENCE, 1 ordered pieces.
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2 (bases )
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 134419)

DOE Joint Genome Institute.
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HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                    Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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1 (bases 1 to 720)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

Direct Submission

Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France

2 (bases 1 to 720)
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Botryotinia fuckeliana
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Botrytis cinerea strain
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17; Conserv
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r 2 4 4 4 5 7 7 205 AACGGCAG V52614 Standa V52614; 21-DEC-1998 21-DEC-1998 21-DEC-1998 21-DEC-1998 21-DEC-1998 21-DEC-1998 21-DEC-1998 CS 21	ര്ജ് ര 🗏	Fujii K, Furutani Fujii K, Furutani WPI: 97-489627/45 P-PSDB; W34320. Novel beta-2 adres agonists and antas Disclosure; Page: This sequence enco invention is a bet approximately 75 page approximately 75 page approximatel	Betta-2 adrend Betta-2 adrend asthmatic did Homo sapiens Key CDS W09735963-A1 02-OCT-1997. 24-MAR-1996; 27-MAR-1996;	1 250 star 250;	144.22	
rd; ccc fi	1999 BP; imilarity Conserva	Fujii K, Furutani Y, K Fujii K, Furutani Y, K WPI: 97-489627/45. P-PSDB; W34320. Novel beta-2 adrenalin agonists and antagonis Disclosure; Page 27-30 This sequence encodes invention is a beta-2 approximately 75 pM ag astrening for agonists	Joo Jp-	tandard; cD	74.7 74.7 74.7 74.7 74.7 72.6	
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an; asthma; beta-agonist iers	513 C; 485 G; ore 19; DB 1; Lengt ed. No. 1.2; Mismatches 0; Ind	tani Y, Kawashima H, Nomura A, Yano K; 7/45. 0. 0. adrenalin receptor sub-type - useful for sc. antagonists and researching asthmatic disea: anecodes the protein of the invention. The particle and adrenalin receptor subtype with Kd 75 pM against 1251-cyanopindrol. The prote agonists and antagonists, which are useful	pe coding sequence. pindrol; agonist; antagonis tiers	ALIGNMENTS 1999 BP.		
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/note= "A to G substitution, results in
to Gly amino acid change"

HOSPITAL

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Fish

JE,

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11-SEP-1998; U03908.
26-FEB-1998; US-811441.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HO
BOUShey H, Chinchilli VM, D
Martin RJ;
WPI; 98-506372/43.
P-PSDB; W75777.
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Disclosure; Page 33-35; 46pp; English.
This cDNA sequence codes for human beta-2-adrenergic
W75777) having an arginine residue at position 16. A
for identifying individuals susceptible to adverse re
                                                                                       27-MAR-1996; JP-072914.
(DAIN) DAINIPPON PHARM CO LTD.
Fujii K, Furutani Y, Kawashima H,
WPI; 97-489627/45.
P-PSDB; W34319.
                                                                                                                                                         W09735963-A1.
02-OCT-1997.
24-MAR-1997; J
27-MAR-1996; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing asthma patients predisposed to adverse beta-
reactions upon regular administration - by identifying
homozygous for allele encoding Arg at position 16 of
Novel beta-2 adrenalin receptor sub-type - useful for screening agonists and antagonists and researching asthmatic diseases claim 5; Page 23-26; 47p; Japanese.

This sequence encodes the protein of the invention. The protein invention is a beta-2 adrenalin receptor subtype with Kd value approximately 75 pM against 125I-cyanopindrol. The protein can
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      n of the of be used
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RESULT
X33329/c
ID X3333
AC X333
AC X3
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asthmatic
Sequence
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11-MAR-1999.
02-SEP-1998;
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x33329;
30-JUN-1999
                                                                                                                                                                                                          Canine beta-2 adrenera; Canine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases e.g. osteoporosis

Example 15; Page 75-76; 118pp; Japanese.

The present invention describes DNA which participates in the regulation of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve as a promoter for prevention and treatment of bone diseases including osteoporosis. The present sequence represents a polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUMU ) SUMITOMO PHARM CO LTD. Fujiwara M, Harada H, Katsumata Ogawa S, Tagashira S;
WPI; 99-243621/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1998; JP-114135.
02-SEP-1997; JP-254250.
15-OCT-1997; JP-299407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA regulating expression of protein, useful as promoter i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEBP2 alpha
PEBP2 alpha
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14-OCT-1998
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              W09735973-A2.
02-OCT-1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
                                                                                                                                                                    Canis
                                                                                                                                                                                                                                                                                    V30468
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                                                                                                                                                                                        hybridisation;
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(VETI-)
                                                                                                                                                                                                                                                                                                                                                                                114 AACGCCAGAGCCTTCTTGC
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                                                                                                                                                                      familiaris
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18; Conservative
                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conser
                                                                                                                                                                                                        beta-adrenergic receptor;
VETIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for agonists and antagonists, diseases. 1400 BP; 304 A; 402 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
ds.
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                                                                                        /product=
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89.5%;
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94
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                                                                                              "beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DF Pred. No. 7.1; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; D
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                tissue;
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treatment of bone
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                                                                                                                                                                                                              probe;
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RESULT V8011/c
ID 11/c
ID 11/c
ID 11/c
ID 01/2
ID 08/2
KW 08/C
C
KW 08/C
C
CC 110/C
CC 08/C
CC
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CC This sequence represent the coding region of the canine beta 2-adrenergic CC receptor (RA-Ca-b2) gene. The sequence was isolated from a CDNA library CC constructed from polyA+ RNA purified from dog brown adipose tissue cells. CC The probe was a 600 bp fragment of the coding region of the human beta-3 CC adrenergic receptor covering the region from the initiation codon to CC transmembrane domain 5 (TM5). The full length insert was cloned into M13 CC or sequencing using primers v30491-v30510. The sequence can then be CC expressed e.g. in a mammalian cell, by subcloning into an expression CC vector such as pCDMA3. The beta-2 receptor can be used in comparative Structure-function studies, e.g. for differential screening of ligands CC specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

SQ Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
                                                                                                     pr factor 0sf2 - useful for, e.g. treatment of osteogenic diseases, in vaccines and for diagnosis

PS Claim 5; Pages 185-187; 273pp; English.

CC This DNA encodes a native 0sf2/Cbfal polypeptide (an osteoblast specific factor-2 encoded by the CBFAl locus). Host cells containing a vector comprising a 0sf2/Cbfal nucleic acid are used for the recombinant cc comprising a 0sf2/Cbfal nucleic acid are used for the recombinant cc production of the protein. The 0sf2/Cbfal has osteoblast-specific transcriptional activity (particularly for treating osteogenic diseases, optionally when expressed from a gene therapy vector). Osf2/Cbfal is also used to raise antibodies, to screen for modulators of its activity; used in vaccines and to detect specific antibodies (for diagnosis of bacterial infections). The Osf2/Cbfal polynucleotides can be used to produce transgenic animals or pluripotent non-human animal cells, while their fragments are used to detect Osf2/Cbfal genes by hybridisation, or as antisense molecules or ribozymes for downregulation of gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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29-MAY-1998; US-080189.
24-MAR-1997; US-048430.
(TEXA) UNIV TEXAS SYSTEI
Ducy P, Karsenty G;
WPI; 99-059837/05.
P-PSDB; W89184.
    Osf2/Cbfal polynucleotides and polypeptides are used for specific transcription of osteoblast-specific genes that have an OSE2 sequence element; to generate an immune response; in binding assays to detect (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osf2/Cbfal polypetide encoding DNA.
Osf2/Cbfal; osteoblast specific factor-2; CBFAl locus; transcriptional;
ostoogenic; gene therapy; modulator; bacterial infection; transgenic;
osteoblast; bone; osteocalcin; collagen; osteopontin; sialoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid expressing the osteoblast-specific transcription factor Osf2 - useful for, e.g. treatment of osteogenic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V80117 standard; DNA; 3334
V80117;
15-MAR-1999 (first entry)
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98-032136/03.
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17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except= (pos:1506. .1508, aa:Gly)
/product= "Osf2/Cbfa1 polypeptide"
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105. .1895
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Pred. No. 44;
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RESULT
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PS Claim 72; Pages 155-156; 273pp; English.

CC The invention relates to an Osf2/Cbfal polypeptide (an osteoblast CC specific factor-2 encoded by the CBFAl locus). Host cells containing a CC vector comprising a Osf2/Cbfal nucleic acid are used for the recombinant CC production of the protein. The Osf2/Cbfal has osteoblast-specific CC transcriptional activity (particularly for treating osteogenic diseases, CC optionally when expressed from a gene therapy vector). Osf2/Cbfal is also CC used to raise antibodies, to screen for modulators of its activity; used CC infections). The Osf2/Cbfal polynucleotides can be used to produce transgenic animals or pluripotent non-human animal cells, while their CC fragments are used to detect Osf2/Cbfal genes by hybridisation, or as antisense molecules or ribozymes for downregulation of gene expression. CC Osf2/Cbfal polynucleotides are used for specific curanscription of osteoblast-specific genes that have an OSE2 sequence CC element; to generate an immune response; in binding assays to detect OSE2 element; for purification of such elements and to induce differentiation of osteoblast progenitors for stimulating formation, growth, replacement compair of bone tissue. Antibodies, optionally, labelled, are used as immunessay reagents for detecting Osf2/Cbfal; in DNA-binding assays to detect OSE2 element; progenitors for stimulating formation, growth, replacement condensity other genes to which Osf2/Cbfal can bind; for affinity of detections of osf2/Cbfal and to one related genes. Also regulatory condensity other genes to which Osf2/Cbfal genes are used to genes, e.g. osteoblast-specific expression of homologous or heterologous condensity. The present sequence represents the nucleic acid sequence considered in the order of the order of
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W0985432-A1.
03-DEC-1998.
29-MAY-1998; U10860.
24-MAR-1998; US-080189.
29-MAY-1997; US-048430.
(TEXA) UNIV TEXAS SYSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1999 (first entry)
Nucleic acid sequence of the Osf2 promoter and 5' UTR.
Nucleic acid sequence of the Osf2 promoter and 5' UTR.
Osf2/Cbfal; osteoblast specific factor-2; CBFAl locus; transcriptional;
osteogenic; gene therapy; modulator; bacterial infection; transgenic;
osteoblast; bone; osteocalcin; collagen; osteopontin; sialoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elements; for purification of such elements and to induce differentiation of osteoblast progenitors for stimulating formation, growth, replacement and repair of bone tissue. Antibodies, optionally, labelled, are used as immunoassay reagents for detecting Osf2/Cbfal; in DNA-binding assays to identify other genes to which Osf2/Cbfal and hind; for affinity purification of Osf2/Cbfal and to clone related genes. Also regulatory sequences (promoter and enhancer) from Osf2/Cbfal genes are used to provide osteoblast-specific expression of homologous or heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid expressing the osteoblast-specific transcription factor Osf2 - useful for, e.g. treatment of osteogenic diseases, vaccines and for diagnosis claim 72; Pages 155-156; 273pp; English.
                    sialoprotein. The present sequence represents of the Osf2 promoter and 5' UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ducy P, Karsenty G; WPI; 99-059837/05.
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RESULT 9
V30458_4
Continuation (5 of 6) o
WP Sequence split into
WP Fragment Name
WP V30458_0
WP V30458_1
WP V30458_3
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02-SEP-1998; J03920.
08-APR-1998; JP-114135.
02-SEP-1997; JP-254250.
15-OCT-1997; JP-299407.
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5851 AACGCCAGAGCCTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUMU ) SUMITOMO PHARM CO LTD.
Fujiwara M, Harada H, Katsumata T, Nakatsuka
Ogawa S, Tagashira S;
WPI; 99-243621/20.
                                                                                                                                                                                                                                                                         6737
                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents DNA which participates in the regula of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve promoter for prevention and treatment of bone diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA regulating expression of PEBP2 all protein, useful as promoter for preve diseases e.g. osteoporosis claim 1; Page 76-85; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEBP2 alpha A gene expression regulating DNA sequence #4. PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                                   mouse or human
Sequence 1390
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17; Conser
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89.5%;
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Pred. No. 48;
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Pred. No. 5
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LOCUS V30458
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treatment of bone
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RESULT
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ID T45143 s.
AC T45143;
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RESULT 10
V30459_4
Continuation (5 of 6) c
WP Sequence split into
WP Fragment Name
WP V30459_1
WP V30459_2
WP V30459_3
WP V30459_3
WP V30459_3
WP V30459_5
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                                                                                                                                                                                                                promoting repair and attachment of cartilaginous tissue - using erg. new fusion polypeptide of link protein and cartilage matrix protein, partic. for treating damage caused by arthritis is Disclosure; Fig 5; 48pp; English.

The sequence shows the human cartilage link protein gene. The link protein can be used in conjunction with a cartilage matrix protein to promote binding of a complex of proteoglycan and hyaluronic acid to collagen. The protein can be used to treat cartilage in joints esp. after damage by arthritis (esp. osteoarthritis) or to promote cartilage matrix formation in vitro to provide materiall for restorative or cosmetic surgery. It also promotes attachment to prostheses, implants, tissue grafts, etc.

Sequence 1400 BP; 378 A; 326 C; 344 G; 352 T;
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Matches 16; Conser
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(GEHO) GEN HOSPITAL CORP.
Binette F, Goetinck PF, To
WPI; 94-248890/30.
P-PSDB; R57350.
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1212
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Q70142;
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04-JAN-1994; U00253
06-JAN-1993; US-001
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ACTGCAGCGCCTTCTTG
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94.1%;
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Pred. No. 60;
0; Mismatches
                                                                                                Score 15.4; I
Pred. No. 65;
0; Mismatches
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standard;

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(first entry)
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biosynthesis

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EP-747483-A2.
11-DEC-1996.
29-MAY-1996; 108556.
09-JUN-1995; EP-10888
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                            P-PSDB;
                                    P-PSDB;
                                          (HOFF) HOFFMANN LA ROCHE HOhmann H, Pagamontes L, WPI; 97-023160/03.
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Key
            W06513;
W06514;
W06515;
W06516;
                                                                  EP-108888
                                                                                                                 /note= "base 8t specification" e 8602. .8604
                                                                                                                                                                              specification"
e 8590
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/note= "base 8590 :
specification"
e 8592
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/note= "bases 8539-8540
specification"
8581
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                                                                                                                                                                                                                                                                    /label= ORF-16
8348. .8349
/*tag= 1
                                                                                              /note= "bases 8602-8604 are specification"
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/note= "base
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/label- Cryz
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                                                                                                                                                                                                                                                                                                                                                                                                                                /product- GGPP
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/label- CrtE
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Query Match Best Local S Matches 16

. Similarity 16; Conser

81.18; 94.18;

Score 15.4; D Pred. No. 77; 0; Mismatches

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Length 8991;

1;

<u>..</u>

Gaps

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infection.

PT infection.

PS Claim 1; Page 1239-1244; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it CC 982 nucleotide sequences isolated from the Enterococcus faccalis genome. CC 12938 to X13919 represent these nucleotide sequences which are primary CC nucleotide sequences, also known as contigs. The computer-based system CC can identify fragments of the Enterococcus faecalis genome with CC commercial importance. The products can be used to detect the presence CC of Enterococcus faecalis in samples. They can also be used for CC diagnosing Enterococcal infection in an animal and monitoring CC progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or CC another related organism, in vivo or in vitro. In particular the constant of the progression of the enterococcus faecalis nucleotide sequences another related organism, in vivo or in vitro. In particular the constant of the progression of the enterococcus faecalis nucleotide sequences another related organism, in vivo or in vitro. In particular the constant of the progression of the enterococcus faecalis nucleotide sequences and the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide sequences constant of the progression of the enterococcus faecalis nucleotide of the progression of the enterococcus faecalis nucleotide of the en
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04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the carotenoid blosynthesis pathway. The sequence was deduced finserts of 6 clones obtd. from genomic libraries e.g. by PCR amplification (see also 745144-45) and use of partial clones to screen the library. The identilies of the gene products (see al w006513-19 and w00871) were detd. by examining carotenoid accumulation in E. coli hosts transformed with deleted variants the gene cluster. The isolated genes can be used in different combinations to produce carotenoids in transformed host cells. Sequence 8625 BP; 1458 A; 2898 C; 2964 G; 1295 T;
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animal feeds
Example 2; Fig 7; 80pp; English.
Example 2; Fig 7; 80pp; English.
Genomic DNA (T45143) of Flavobacterium sp. R1534 includes genes
Genomic DNA (T45143) of Flavobacterium sp. R1534 includes genes
Genomic DNA (T45143) of Flavobacterium sp. R1534 includes genes
Genomic DNA (T45143) of Flavobacterium sp. R1534 includes genes
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Genomic DNA (T4514444) of Fl
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Enterococcus faecalis; contig; detection; Enterococcus faecalis; computer readable medium; ds.
Enterococcus faecalis.
MO9850555-A2.
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p-psdB; w06519.
Flavobacterium gene sequences encoding carotenoid biosynthesis
enzymes - for the production of carotenoid(s), useful in foods and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch
WPI; 99-045171/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4503 ACGGCAGCGCCTTCTCG 4487
   Sequence
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                                           Infection.
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94.18;
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Pred. No. 76;
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8630 AATGGCAGCGCCTTCTT

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RESULT 1
T87401/c
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В
                              W09634099-A2.

31-OCT-1996.

29-APR-1996. CA0263.

28-APR-1995. US-431048.

28-JUN-1995. US-436841.

31-JUL-1995. US-509359.

A (HSCR-) HSC RES & DEV LP.

A (UTOR) UNIV TORONTO GOVERNING COUNCIL.

A (UTOR) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9707213-A2.
27-FEB-1997.
15-AUG-1996; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, cancer and ageing
claim 16; Fig 1; 77pp; English.

Claim 16; Fig 1; 77pp; English.

Identifying genes which cause improper chromosome segregation, screening for inhibitors of chromosome missegregation and procueus given in T87401 to T87426 can be used in the above methods. Given in T87401 to T87426 can be used in the above methods. It is not clear from the figure legend, the figure and the disclosure of the specification which sequence of Fig 1 and Fi is the And/AD3LP or the An3 sequence.

Sequence 1417 BP; 307 A; 385 C; 380 G; 345 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
Li J, Potter H;
WPI; 97-165297/15.
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07-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W28506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     presenilin; inhibitor; AD;
                                                                                                                                                                                                                                    T40031;
25-JUL-1997 (first entry)
25-JUL-1997 (first entry)
Human presenilin-2 wild type coding sequence.
Presenilin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein;
familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                       1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying genes which ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD3; AD4/AD3LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AD4/AD3LP sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187401 standard; DNA; 1417
         Fraser PE, Rommens WPI; 96-497631/49. p-PSDB; W05762.
                                                                                                                                                                                                                         depression; antibody; gene expression modulator;
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                      T40031 standard; DNA; 2229
 New
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presenilin genes - useful
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                                                                                                                                                                                                                                                                                                                                                                                 ggcagcgccttcttg 18
                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; chromosome; missegregation; ibitor; AD; trisomy 21; ss.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cause chromosome missegregation - useful for ad treatments for diseases, e.g. Alzheimer's {\bf r}
                                                                                                                                                            presenilin-2
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0; Mismatches
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                                       George-Hyslop
  for diagnosis, therapy
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o. le+02;

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     and drug
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pr screening of familial Alzheimer's disease, cerebral disorders, etc. ps Claim 8; page 148-150; 178pp; English.

CC Taim 8; page 148-150; 178pp; English.

CC T40028 and T40029 represent the coding sequences for the human presenilin-2. CC T40029 results from alternate splicing of the genomic DNA sequence CC T40029 results from alternate splicing of the genomic DNA sequence. CC T40030 represents the coding sequence for wild type mouse ps-1. The CC presenilins are a family of highly conserved integral membrane proteins CC with a common structural motif, common alternate splicing patterns, and CC common mutational hot spot regions. Mutations in PS genes are implicated CC common mutational hot spot regions. Mutations in PS genes are implicated CC in familial Alzheimer's disease (AD) and possibly other diseases such as CC cerebral haemorrhage, schizophrenia, depression etc. so detection of CC cerebral haemorrhage, schizophrenia, depression etc. so detection of CC antisense sequences, antibodies selective for mutant forms of thee encoded proteins (such as W05736) and modulators of PS gene expression are useful ptentially useful for treatment of AD etc. Transgenic animals are useful CC affinity purification and in immunoassays.

SQ Sequence 2229 BP; 481 A; 579 C; 633 G; 521 T;
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Best Local S
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1606 GGCAGCGCCTTCTTG
                            4 ggcagcgccttcttg
                                                                                         15;
                                                                                                            Similarity
                                                                                         Conservative
                                                                                                              78.9%;
       1592
                                               18
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Pred. No.
                                                                                              Mismatches
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                                                                                                                                      Length 2229;
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Search completed: September Job time: 4099 sec 12, 2000, 23:07:17 THIS PAGE BLANK (USPTO)

Run

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OM nucleic -

Title: Perfect score:

Sequence

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Total number of hits satisfying chosen parameters:
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3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

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; GENERAL INFORMATION:
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; LOCATION:
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AMAE: MBK1, DAVID J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 99000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-622-6031

TELEFAX: 3723836

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENCTH: 1242 base pairs
   Query Match
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Matches 19
                                                                                                                                                                                                                                                                                  STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CITY: Seattle
STATE: Washington
COUNTRY: United St
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FILING DATE: 19910208
CLASSIFICATION: 435
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US-08-460-490-1
US-08-460-490-1
US-08-462-728-3
PCT-US92-00730-1
PCT-US92-00862-1
US-08-557-309B-19
US-08-657-36-1
US-08-6814-06-19
US-08-6816-444-1
US-08-686-444-7
US-08-866-444-7
PCT-US92-454A-2
US-08-866-715-1
US-08-686-715-1
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   Score 19; DB 6
Pred. No. 0.83;
Mismatches
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                                                                     DB 6;
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Searched:

Scoring table: Sequence:

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US-08-001-078A-2/c
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US-08-463-218-2/c
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TOPOLOGY:
US-08-001-078A-2
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                 Sequence 2, Application US/08463218 Patent No. 5986052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227.7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tondravi, M., Mehrdad APPLICANT: Binette, Francois TITLE OF INVENTION: METHODS FOR ITITLE OF INVENTION: FORMATION UNMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                   APPLICANT: Goetinck, Paul F.
APPLICANT: Tondravi, Mchrdad
APPLICANT: Binette, Francois
TITLE OF INVENTION: MCTHODS FOR PROMOTING CARTILAGE MATRIX
TITLE OF INVENTION: FORMATION
                                                                                                                                                                                                                                                                                                               1212 ACTGCAGCGCCTTCTTG 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goetinck, Paul F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 06-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                   STREET:
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BOSTON
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60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binette, Francois
NVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
                 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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94.1%;
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1212 ACTGCAGCGCCTTCTTG 1196

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; Sequence 2, Application PC/TUS9400253

; GENERAL INFORMATION:
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                                                                                                                        Matches
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Best Local :
                                          Matches
                                                          Query Match
Best Local Similarity
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APPLICATION NUMBER: US/08/463,218
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,078
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
RECISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-008DV
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 06-JAN-1993 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DO:
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1212 ACTGCAGCGCCTTCTTG 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: ASCII text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                  LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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2 acggcagcgccttcttg 18
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SYSTEM: PC-DOS/MS-DOS
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94.1%;
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                                                            Score 15.4;
Pred. No. 42;
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Pred. No. 4
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US-08-888-077A-18/c
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Patent No. 5985564
GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 18, Application US/08888077A Patent No. 6020143
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserva
                                                                 GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan Esq., Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 1047 GCCAGCGCCTTCTTG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan Esq., Patricia
REGISTION NUMBER: 32,727
REFERENCTION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                    DDRESSEE:
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2: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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PENTION: ASSAY FOR IDENTIFYING GENES CAUSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%;
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64;
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; LOCATION: 1.2226
; OTHER INFORMATION: /note= "hPS2"
US-08-888-077A-18
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-875-972-28/c
                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/08875972 Patent No. 5985564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 15;
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APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
RECISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908) 654-7866 INFORMATION FOR SEQ ID NO:
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1606 GGCAGCGCCTTCTTG 1592
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LENGTH: 2229 base pair
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                          STREET: Two Mil-
CITY: Lexington
STATE: Massachus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
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LOCATION:
                             APPLICATION NUMBER: FILING DATE: 08-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-JUL-1997 CLASSIFICATION: 530
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STATE: NJ
                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                          02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 78.9%; Score 15; Similarity 100.0%; Pred. No.
                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                               Two Militia Drive
                                                                                                                                                                                             USA
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366..1712
08-AUG-97
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FILING DATE: 16-AUG-1995 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 6 FILING DATE: 16-AUG-1995

US 60/002,448

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granahan Esq. Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEPACE: (781) 861-9540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 2276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 136,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                            TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1648 GGCAGCGCCTTCTTG 1634
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-NOT CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: High
CITY: Boston
                  TOPOLOGY:
                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                 H: 2285 base pairs nucleic acid
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                                                                                                                                                                                                                                                                      umber: US/08/967,101
10-NOV-1997
                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
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                                                                                                                                                                                                                            08/592,541
                                                                                                       136:
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RESULT 10
US-08-651-136C-63
; Sequence 63, Application US/08651136C
; Patent No. 6001639
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 136:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 100.0%;

Matches 15; Conservative
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Best Local Similarity
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                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
FILING DATE:
                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1606 GGCAGCGCCTTCTTG 1592
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                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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      APPLICANT:
                                                                                                                                                                                         APPLICANT:
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ggcagcgccttcttg 18
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 2285 base pairs
nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598605
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08592541
                                                            Kauppinen, Markus
Lange, Lene
                                                                                                                      Andersen, Lene N.
Lassen, Soren F.
                                                                                                                                                                             Schulein, Martin
Ihara, Michiko
                                   Nielsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEORGE-HYSLOP, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800
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Pred. No.
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66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.8
---- 15; Conservative
                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08270013B Patent No. 5686294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-867-01:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/270,013B
                                                                                                                                                                                                                         APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RES
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Loydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
APPLICATION NUMBER: US/01
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Le
CITY: New York
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                 STREET: Two Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 CGGCAGCGCCTTCATG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                                                                                               61601-6780
                                                                                                                                                                                                 Illinois
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                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takagi, Shinobu
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                                                                                                                                                                                                                                                                                                       PROTEIN HAVING HEAT-RESISTANT MALATE DEHYDROGENASE ACTIVITY
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93.8%;
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Pred. No. 1
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RESULT 12
US-08-838-418-1
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TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEEX: (25)3533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 15; Conserv
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          APPLICATION NUMBER: US 08/270,013
FILING DATE: 01-70L-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-70L-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOOVET, Allen E.
REGISTRATION NUMBER: 37354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1361 AACGGCAGCGCCTACT 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sogabe et al. TITLE OF INVENTION: PROT TITLE OF INVENTION: DEHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
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ANTI-SENSE: NO
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/838,418 FILING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Pa
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 aacggcagcgccttct 16
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REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                          60601-6780
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93.8%;
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Pred. No. 1
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TELEX: (25)3533 INFORMATION FOR SEQ'ID NO:

TELEFAX:

(312) 616-5700

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US-08-220-240A-4
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Best Local S
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 29 MAR-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
STRAIN: ATCC12016
               TELEFAX: (312) 474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTIBODIES RECOGNIZING TIE RECEPTOR TITLE OF INVENTION: TYROSINE KINASE AND USES THEREOF NUMBER OF SEQUENCES: 5
                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 09-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                           FILING DATE: 08-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
SEQUENCE CHARACTERISTICS:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                           APPLICATION NUMBER: US 08/167,453 FILING DATE: 15-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                               REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TRY: Unites States of America 60606-6402
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                                                                                                            Gass,
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matikainen, Marja-Terttu
Partanen, Juha
Makela, Tomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Korhonen,
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                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                        David A.
David R. 38,153
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93.8%;
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Pred. No. 1.3e+02;
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US-08-220-240A-4
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                                                                    US-08-384-106A-8
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Best Local (
          Query Match
Best Local Similarity
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Matches
                                                                                                                                                                                                                                                                                                                               SOFTWARE: PATENTIN Releating Reprication DATA:
APPLICATION NUMBER: US/V
FILING DATE: 06-FEB-199-
CLASSIFICATION: 435
                                                                                                                                                                                                                 TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: INK4c-p18 and INK4d-p19, Inhibitors of TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                FEATURE:
                                                                                                                              MOLECULE TYPE:
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Local Similarity 93.8%;
es 15; Conservativo
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                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington
                                                                                  NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                       LENGTH: 501 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okuda, Tsukasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Hirai Ph.D., Hiroshi
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 Conservative
                                                                                                                                             linear
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               74.78;
84.28;
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Pred. No. 1.
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 Score 14.2; DB 5;
pred. No. 1.4e+02;
0; Mismatches 3;
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                               Length 501;
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FEATURE:

NAME/KEY:

LOCATION:

PCT-US96-01643-8
Search completed: September 12, 2000, 23:04:32 Job time: 3939 sec
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APPLICATION NUMBER: PCT/US96/01643
FILING DATE: 06 FEB-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/384,106
FILING DATE: 06 FEB-1995
CLASSIFICATION:
APPLICATION NUMBER: 995
CLASSIFICATION:
APPLICATION:
BEGUENCE CHARACTERISTICS:
APPLICATION:
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Sequence 8, Application PC/TUS9601643

GENERAL INFORMATION:

APPLICANT: St. Jude Children's Research Hospital

TITLE OF INVENTION: InK4c-pl8 and InK4d-pl9, Inhibitors of

TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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Best Local Similarity 84.2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens POSITION IN GENOME: CHROMOSOME/SEGMENT: p19
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MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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84.2%; Pred. No. 1.4e+02;
tive 0; Mismatches 3
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                                                                                                                                                                                                                                                                   National Cancer Institute / Nation
Disorders and Stroke, Brain Tumor
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACGGCAGCGCCTTCTTGC
             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1052 Std Error: 0.00
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AI475044
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1 (bases 1 to 195)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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                                                                                                                                                                                                                                                 Tissue Procurement: David
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/db_xref="taxon:9606"
/clone="GEN-559E06"
/clone_lib="Human placenta cDNA (TFujiwara)"
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Shimada,Y.,
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                                                                                                                                                                                                                                                 M.D.,
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RESULT
C18250/c
                    DEFINITION
C18250 377 bp mRN
C18250 Human placenta cDNA
GEN-559E06 5', mRNA sequenc
   mRNA sequence.
                                   mRNA
                   (TFujiwara) Homo
                 sapiens cDNA clone
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ALIGNMENTS

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AI836000 AQ803246 AW533116 AW186808

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AI844706 AI390851 AW046979

AI836840

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R86510 AU046197 AW036224 AI835798 AI846942 AI846943043 AI846942 AI848899 AI848899 AI836035 W150035 AW493285

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AW491133

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AI828151 AI939616 AA234907 AA150236 N27820

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Best Local
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UI-H-BII-aeb-b-10-0-UI.s1 NCI_CGAP_Sub3
IMAGE:2718667 3', mRNA sequence.
AWl39725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq prime
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jun 22, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="Ibxon:9606"
//clone=lib="NCI_CGAP_Sub3"
//lab_host="DH10B (Life Tenhnologies)"
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87 c 51 g 29 t
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/db_xref="taxon:9606"
/clone="IMAGE:2162716"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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REFERENCE
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AI128872
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KEYWORDS
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ORIGIN
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                                                                          Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleoston Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/nclegap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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qf16g08.sl NCI_CGAP_Brn25
mRNA_sequence.
                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
On May 18, 1998 this sequence version Contact: Robert Strausberg, Ph.D.
Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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AI128872.1 GI:3597386
                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_LL1, NCI_CGAP_Lei2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_LL1, NCI_CGAP_Lei2,
NCI_CGAP_Br3, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Br3, NCI_CGAP_Co8, NCI_CGAP_Co8,
NCI_CGAP_Br3, NCI_CGAP_GC6, NCI_CGAP_GC6,
NCI_CGAP_Br3, NCI_CGAP_GC6, NCI_CGAP_GC6,
NCI_CGAP_Br3, NCI_CGAP_GC6, NCI_CGAP_GC6,
NCI_CGAP_Lu19, NCI_CGAP_GC6, NCI_CGAP_GC6,
NCI_CGAP_Kid3, NCI_CGAP_Lid5 below:
NCI_CGAP_Kid3, Pool 1 LLAM, 334-337, 3682-3683,
3798-3803 (LMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1
1LAM, 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lu5 pool 1 LLAM, 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_EC64
pool 1 LLAM, 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_PT22 pool 1 LLAM, 2647-2459,
1101192-1101959, 1217928-1220615); NCI_CGAP_CO10 pool 1
1LAM, 2644-2653, 2871-2872 (LMAGE CloneIDs 1057416-1061255,
1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches 70 Facilitate Gene Discovery. Genome Research 6, 791-806.;

TAG_LIB-NCI_CGAP_PT22; TAG_TISSUE-prostate; TAG_SEQ-AAGTG"
34 a 128 c
                                                                                                                                                                                                                                                                                                                   (301) 496-1550
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94.78;
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Pred. No. 1.1e+02;
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                                                                                                     Sequencing Center information can be
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AI199676
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Best Local (
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
On Oct 6, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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AI199676
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                                                                                                                                                                      Seq primer: -40UP from Gibco
                                                                                                                                                    quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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/clone="IMAGE:1860856"
/clone_lib="NCI_CGAP_Brn25"
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/clone="IMAGE:1750238"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/lab_host="DH10B"
                                                                                              /organism="Homo sapiens"
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94.7%;
                                                                                                                                ion/Qualifiers
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Nov 2, 1998 this sequence version replaced gi:3829848 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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wk32f10.x1 NCI_CGAP_Brn25
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                                                                                                                                                                                                                                                                              Seq primer: -40UP from Gibco
High quality sequence stop: 4
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Ph.D.
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                               quality sequence stop: 440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
Procurement: David N. Lou
adaptors (Pharmacia), digested with Not I at the Not I and Eco RI sites of the modified Library is normalized, and was constructed
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192 c 138 g 58 t
                                                                                                                                                 /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2414059"
/clone_lib="NCI_CGAP_Brn25"
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                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
On Oct 13, 1998 this sequence version replaced gi:3738881.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NRIJONAL Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
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tm62e03.x5 NCI_CGAP_Brn25 Hor
                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 1052
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Tissue Procurement: David N. Lou
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D.
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         /clone="IMAGE:2162716"
/clone_11b="NCI_CGAP_Brn25"
/tlssue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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information can be
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IMAGE:2162716 3';
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hilller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to
AA234907
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zs38f03.rl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
           /note-*Organ: mixed (see below); Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.*
                                                                                                                                                                                                                                                                                                         /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:687485"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:5591635"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                   'lab_host="DH10B"
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Pred. No. 1.
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Best Local Query Match

l Similarity 16; Conserv

Conservative

84... 100.0%; Fi

Score 16; Pred. No.

DB 23; 1

Length 422; Indels

0;

Gaps

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Mismatches

Matches

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AA150236/c
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                           cggcagcgccttcttg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hakkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Hawkins, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA150236 423 bp mRNA EST 14-MAY-1997 z103c01.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491232 5' similar to TR:G1213518 G1213518 ALG3 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 825 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
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4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                          82
                                                               Conservative
                                                                                                                                                   Eutheri
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:3805819"
/db_xref="taxon:9606"
/clone="IMAGE:491232"
                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
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                                                                           84.2%;
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Primates;
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                                                                              Score 16;
Pred. No.
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                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                              DB 22; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo, M.F., Chiapelli, B., T., Favello, A., Gish, W.,
                                                                                               Length 423;
                                                                    Indels
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N27820/c
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N27820.1
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1 (bases 1 to 498)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N27820 498 bp mRNA EST 30-DEC-1:
yx54h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:265603 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 220
Source: IMAGE.Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
   R86608
R86608.1
                                                                                                                                                                                                                              l Similarity
16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                 R86608 195 bp mRNA EST 17-AUG-1995 RABEST229T RAbbit Osteoclast, Dennis Sakai Oryctolagus cuniculus CDNA clone pRABOC229 5' similar to cofilin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 220.
Location/Qualifiers
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino. 125 c 137 g 131 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĢI:1142301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:265603"
/clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:3875245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
     GI:947286
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                                                                                                                                                                                                                                                   84.2%;
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                                                                                                                                                                                                                                                     Score 16;
Pred. No.
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                                                                                                                                                                                                                                    DB 86; I
5.3e+02;
hes 0;
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                                                                                                                                                                                                                                                                     Length 498;
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DEFINITION
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AI413640
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                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                   aacggcagcgccttcttgc 19
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 197)
1 (bases 1 to 197)
                                                                                                                                                                                                                    AI413640 197 bp mRNA EST mb29h12.x1 Soares mouse p3NWF19.5 Mus musculus IMAGE:330887 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 10, 1995 this sequence version replaced gi:805895. Other EST8: RABEST038T, RABEST045T, RABEST103T, RABEST
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96021365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 195)
Sakal, D., Tong, H. S. and Minkin, C.
Ostcoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Southern California USC School of Dentistry, 925 West 34th Angeles, CA 90089-0641 Tel: 2137405563
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Email: sakai@molbio.usc.edu
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/db_xref="taxon:9986"
/clone="pRABOC229"
/clone_llb="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH125"
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Pred. No. 6.2e+02;
0; Mismatches 2;
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AUTHORS
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Best Local Similarity
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1 (bases 1 to 234)

Sakai,D., Tong,H.-S. and Minkin,C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)

96021365

On May 10, 1995 this sequence version replaced gi:805875.
Other_ESTS: RABEST308T, RABEST304T, RABEST103T, RABEST140T, RABEST302T, RABEST308T, RABEST30
                                   University of Southern California
USC School of Dentistry, 925 West 34th Street,
Angeles, CA 90089-0841
Tel: 2137405563
Fax: 2137407560
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RABEST163T Rabbit Osteoclast, Dennis Sakai Oryctolagus cunicu
CONA clone pRABOC163 5' similar to cofilin, mRNA sequence.
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Email: mouseest@watson.wustl.edu
This clone is available royalty/free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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Oryctolagus cuniculus.
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//dev_stage="19.5 dpc total fetus"
//lab_host="DH10B (ampicillin resistant)"
//lab_host="DH10B (ampicillin resistant)
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sakai@molbio.usc.edu
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/db_xref="taxon:10090"
/clone="IMAGE:330887"
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1 (bases 1 to 235)
Sakai, D., Tong, H.-S. and Minkin, C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
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Seq primer: T7 promoter
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                                                                                                                                                                                                      Insert Length: 629 Sto
Seg primer: T7 promoter
                                                                                                                                                                                                                                                                                                  Angeles, CA 90089-0641
Tel: 2137405563
                                                                                                                                                                                                                                                                                                                                           University of Southern California
USC School of Dentistry, 925 West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone 17 (2), 111-119 (1995)
                                                                                                                                                                                High quality sequence stop: 233.
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/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-Not1 anchor-primer and second strand
with an oligo(dT)-Not1 anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of Sal1 adapters and Not1 digestion, the cDNA was
cloned between the Sal1 (50) and Not1 (30) sites of the
pSPORT1 (BRL) plasmid vector."

57 a 62 c 81 g 34 t
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                                                                                                                                                                                                                                                                                 2137407560
                                                                                                                                                                                                                                                      : sakai@molbio.usc.edu
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/strain="New Zealand White"
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                                                                 /strain="New Zealand White"
/db_xref="taxon:9986"
                                                                                                                                                             Location/Qualifiers
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
                                           /clone="pRABOC140"
                                                                                                                 /organism="Oryctolagus cuniculus"
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                                                                                                                                                                                                                                Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 89
Pred. No. 6.3e+02;
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Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 275)
Sakai,D., Tong,H.-S. and Minkin,C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jan 5, 1998 this sequence version replaced gi:1269075. Other ESTs: RABEST038T, RABEST045T, RABEST084T, RABEST140T, RABEST163T, RABEST202T, RABEST229T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: sakai@molbio.usc.edu
Insert Length: 737 Std Er:
Seq primer: T7 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angeles, CA 90089-0641
Tel: 2137405563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Sakai D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basic Sciences
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Location/Qualifiers
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/clone_lib="Rabbit Ostooclast, Dennis Sakai"
//lab_host="E. coli DH12S"
//lab_host="E. coli DH2S"
//note="vector: pSpORTI; Site_1: SalI; Site_2: NotI;
//note="vector: pSpORTI of DH2SIZE of Depulation of Poly And SalI of DH2 was synthesized by priming with an oligo(dT)-NotI anchor-primer and second strand with an oligo(dT)-NotI anchor-primer and second strand cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of SalI adapters and NotI digestion, the cDNA was cloned between the SalI (50) and NotI (30) sites of the pSPORTI (BRL) plasmid vector."
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                                                                                                                                                                                                                                                                                                                                           /strain="New Zealand |
/db_xref="taxon:9986"
/clone="pRABOC103"
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
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Maximum Match 100%
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Maximum DB seq length: 1000000
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1: gb_bal:
2: gb_ba2:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16.4	16.4	17.4	17.4	17.4	17.4	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	Score
86.3	86.3	91.6	91.6	91.6	91.6	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
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x59939 E.coli ORF1	AJ011615 Zea mays	AC019279 Homo sapi	AC019007 Homo sap1	AF000134 Sus scrof	286037 B.taurus mR	AC011334 Homo sapi	AC011354 Homo sapi	J02960 Human beta-	M15169 Human beta-	A65720 Sequence 1	Y00106 Human gene	X04827 Human mRNA	X94608 C.familiari	AF192345 Felis cat	L38905 Macaca mula	U73206 Canis famil	AF203386 Homo sapi	AF169225 Homo sapi	AF202305 Homo sapi	AF022956 Homo sapi	AF022955 Homo sapi	AF022954 Homo sapi	AF022953 Homo sapi	Description

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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic recein normal and asthmatic subjects in normal and asthmatic subjects in promatical and asthmatic subjects in promatical subjects in subjects in promatical subjects in promatical subjects in promatical subjects i
                                                                                                                                                                                                                                                                            Green, S.A., Turki, J., Innis, M. and Liggett, S.B. Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
                                                                                                                                                                                                                                                                                                                                                                    properties of the receptor J. Biol. Chem. 268 (31), 2:
                                                                                                                                                       Submitted (04-SEP-1997) Medicine, Univ of Cincinnati, Ave ML670564, Cincinnati, OH 45267-0564, USA
                                                                                                                                                                                                                  Erratum:[[published erratum appears in 29;33(47):14368]]
4 (bases 1 to 1242)
                                                                                                                                                                                                                                                                                                                                                                                               Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional
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/product="beta2-adrenergic receptor"
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                              /gene="ADRB2"
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A polymorphism of the human beta 2-adrenergic rece
fourth transmembrane domain alters ligand binding
properties of the receptor
J. Biol. Chem. 268 (31), 23116-23121 (1993)
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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects
in normal and asthmatic subjects
in pormal and asthmatic subjects
in gene (2018)
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Liggett, S.B. and Green, S.A.
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29;33(47):14368]]
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/note="Arg16 to Gly p
/replace="a"
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory proper blockemistry 33 (32), 9414-9419 (1994)
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Liggett, S.B. and Green, S.A.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
                                                                                                                     Submittèd (04-SEP-1997) Medicine, Univ of Ave ML670564, Cincinnati, OH 45267-0564, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           Green, S.A., Turki, J., Innis, M. and Liggett, S.B. Amino terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist t-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
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Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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1 (bases 1 to 1242)
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Liggett, S.B. and Green, S.A.
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29;33(47):14368]]
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1242
/gene="ADRB2"
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IIMGTETLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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NEWCEEWTSIDVLCVTASIETLCVIAVDRYFALTSPEKYGSLITKNKARVILILAVUV
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/note="Val34 to Met polymorphism"
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/protein_id="AABB2150.1"
/db_xref="GI:2570531"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1286)
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Rupert, J.R. and Hochachka, P.W.
Beta-2-adrenergic receptor allele frequencies in two native
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Homo sapiens beta-2-adrenergic receptor gene, complete
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Rupert, J.R. and Hochachka, P.W.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IIMGTFTLCWLPFFIVNIVHYIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="5q31-q33"
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/tissue_type="blood"
                                                                                                                                                                                                                                                                             /replace="C/T"
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/db_xref="taxon:9606"
/chromosome="5"
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Submitted (09-NOV-1999) Zoology, Use Control (19-NOV-1999) Zoology, 
                                                                                                                                                                                     complete cds.
U73206
U73206.1 GI:1657819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1290)
Rupert, J.L. and Hochachka, P.W.
Beta 2 adrenergic receptor allele frequencies in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1290)
Rupert, J.L. and Hochachka, P.W.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherla; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 1298)
                                                                                                                       Canis familiaris
                                                                                                                                                                                                                                                                Canis
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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                      Huang, R.R., Rapoport, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MG0PGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVEGNYLVITAIAKEERLOTVINVEITSLACADLVMGLAVVPGAAHILMKWTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPEKVGSLITKNKARVILMKWUFV
SGLTSFLPIOMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
YSRVFOEAKROLOKIIKSEGRRHYQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTETLCWLPFFIVNIVHVIQDNLIRKEVYILLMMIGYVNSGFNPLIYCRSPDFRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="beta-2 adrenergic receptor"
/protein_id="AAF20199.1"
/db_xref="GI:6636496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="5q32-q34"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="catecholamine receptor"
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26. .1267
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Pred. No.
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                      Schaeffer, M.T.,
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, BC V6T 1Z4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                           receptor (dogbeta2) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                        Cascieri, M.A.
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                                                                                              Mammalia;
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ORGANISM
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TITLE
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Amend, A.M. and Guan, X.M.
Cloning, sequencing, and expression of adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACBZAR 1320 bp mRNA PRI 02-OCT-1995 Macaca mulatta beta-2 adrenergic receptor (B2AR) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning
J. Recept. Signal
97364078
                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta
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beta-2 adrenergic receptor.
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                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta cDNA to mRNA.
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ang,R.-R.C., Rapoport,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSAFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSNNSNSRSDYAGEHSGCHLGQEKDSELLCEDPPGTEDR
GCTVPSDSVDSQCRNCSYNDSLL*
a 396 c 359 g 283 t
                                                                                                                                                                                                                                                      Biol. 14 (9),
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LAIVFGNVLVITAIARFERLQTVTNYFITSLACADLVMGLAVVPFGASHILMKMWTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVVILMVWIV
SGLTSFLPIQMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSFVLPLVVMVFV
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/protein_id="AAB93647.1"
/db_xref="GI:1657820"
/gene="B2AR"
1. .1320
                                                                                                       to be identical with the cDNA"
                                                                                                                                            /organism="Macaca mulatta"
/db_xref="taxon:9544"
                                                                                                                                                                                          Location/Qualifiers
1. .1320
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/db_xref="taxon:9615"
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                                                           /gene="B2AR"
                                                                                                                             /note="genomic DNA for this receptor sequenced
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                                         .1320
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Pred. No.
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                                                                                                                                                                                                                                                                                                monkey beta
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BASE COUNT
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ORGANISM
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BASE COUNT
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Best Local S
Matches 19
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Felis catus |
AF192345
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19; Conserv
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Cully,D.F., Tremm1,G. and Zachwieja,S.
Direct Submission
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Cully,D.F., Tremm1,G.
Felis domesticus beta
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Eukaryota;
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Eutheria; Carniyora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-OCT-1999) MRL, Merck & Co.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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/product="Peta-2 adrenergic receptor"
/product="Neta-2 adrenergic receptor"
/product="Neta-2 adrenergic receptor"
/product="Neta-2 adrenergic receptor"
/product="Neta-30 adrenergic receptor"
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/translation="McOpGNGSAFLLAPNGSHAPDHDVTQERDEAWVVGMGIVMSLIV
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SGLTSFIDIOMHWYRATHQEAINCYAKETCCDFFTNOAVALALSIVSETVPLVIMVFIV
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AFQELLCLRRSSLKACGNGYSSNSNNTGEQSGYHLEQEKENKLLCEDLPGTEDFVGH
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1289. .1320
/gene="B2AR"
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41. .1288
                                   /product="beta-2 adrenergic receptor"
/product="beta-2 adrenergic receptor"
/product="beta-2 adrenergic receptor"
/product="beta-2 adrenergic receptor"
/product="de-"adr04304.1"
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IAFQELLCLRRSSLKAYGNGYSNNSNSRFDYAGEHSGGPLGQEKDSEVLCEDPPGTENL
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    AFQELLCLKKSSUMMET TO THE ANROGIVPNDSIDSQGQNGSTNDSLL"
APA 9 398 g 372 t
                                                                                                                                                                                                                                                                                                                                               /note="synonym: Felis domesticus"
<6. .>1262
                                                                                                                                                                                                                                                               receptor subtype
                                                                                                                                                                                                                                                                                                                      /product="beta-2 adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Felis catus"
/db_xref="taxon:9685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Carnivora; Fissipedia; Canidae; Canis.
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Direct Submission
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19; Conserv
Human mRNA for brain
x04827
x04827.1 GI:29372
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7. Anim. Sci. 74 (9), 2285 (1996)
                                           HSBARR
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ala, C.W., Kuhl, J., Hirshman, C.A. and Levine, M.A.
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nilarity 100.0%;
Conservative 0;
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LAIVFGNVLVITAIARFERLQTVTNVFITSLACADLVMGLAVVFGASHILKKMWTFG
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YSRVFQVAQRQUQKIDRSEGRFHAQNLSQVEQDGRSGHGHRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVJQDNLIPKEVYYILLNWYGYVNSAFNPLIYCRSPDFRI
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/db_xref="GI:1359589"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Canis familiaris"
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for beta2-adrenergic receptor.
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1 (bases 1 to 1970)
Chung, F. Z., Lentes K.U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors
FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerlavage, A.R.
Direct Submission
Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases
                               Human gene for bete
Y00106
Y00106.1 GI:29370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substantial corrections are reported in [2]
Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
Location/Qualifiers
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                                                                2305 bp DNA
gene for bota-adrenergic
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/note="pot.
1502..1507
/note="pot.
1952..1957
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/translation="McQPGNGSAFILAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIV
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NEWUFWSGLTSFUPLCYMWYRATHQEALNCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
YSRVFQEAKRQLQKIDKSEGREHYQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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1459. .
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TVPSDNIDSQGRNCSTNDSLL"
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/note="pot. glucocorticold-responsive element"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                       'note-"pot. polyA signal"
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unidentified.
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1 (bases 1 to 2305)
Schofield, P.R., Rhee, L.M. and Peralta, E.G.
Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                               Sequence 1 from Patent A65720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-OCT-1987) to the EMBL/GenBank/DDBJ databases Location/Qualifiers
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Schofield, P.R.
                                                                            A65720.1
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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1712. .1774
/note-"membrane spanning domain VII"
1 616 c 649 g 545 t
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF Patent: WO 9735973-A 02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta-2-adrenergic receptor mRNA, M15169 J02728 M16106 M15169.1 GI:178201
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                                                                                                                                                                                                                                                                                                                                                                   cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)
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Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
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87222338
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Compugen Ltd
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Canine beta-2 adre
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F gene coding se
mman glial cell
                        RESULT 2
Q13383/C
ID 913383 standard; DNA; 191 BP. AC 013383;
DT 07-NOV-1991 (first entry)
DE 2C2719 oligonucleotide (pHRS17)
KW AR; addrenergic receptor; G-proip W09112273-A.
PD 22-AUG-1991; U00909.
PR 08-FEB-1991; U00909.
PR 08-FEB-1990; US-478100.
PA (ZYMO-) ZYMOGENETICS INC.
PI Sledziewsk AZ, Sheppard PO; DR WPI; 91-267100/36.
PT producing hybrid G-protein couppt sequences encoding receptors he
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requences encoding receptors having at least one domain replaced
by corresp. yeast domain used to transform yeast host cells
by corresp. yeast domain of the STE2 gene prod. contiguouslectides 2C2719 and 2C2720 (013383-84) were designed to
configuration of the STE2 gene prod. contiguouslectides 1-147 of the
x-terminal domain of the STE2 gene prod. contiguouslectides 1-147 of the
yeast G protein-coupled protein gene joined to nucleotides 103-136 of
the human G protein-coupled protein gene (see 013381).
The oligonucleotides, the beta2AR fragment and the pWNR1 vector
fragment were joined in a four-part ligation, to construct pHRS15.
From pHRS16, construct pHRS16 is produced encoding the human beta2-
see also 013381 and 013383-83.
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Q13384;
Q7-NOV-1991 (first entry)
ZC2720 oligonucleotide (pHRS17).
AR; adrenergic receptor; G-protein
W09112273-A.
22-AUG-1991.
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AR; adrenergic receptor; G-prote-
W09112273-A.
22-AUG-1997
WPI: 91-267100/36.

Producing hybrid G-protein coupled receptors - mammalian DNA sequences encoding receptors having at least one domain replaced
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08-FEB-1990; US-478100.
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Pred. No.
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Rat NDF clone 20 D
Rat NDF clone 11 D
Rat NDF clone 19 D
Urea transporter p
Rat NDF clone 42 B
Rat NDF clone 22 D
Rat NDF clone 22 D
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producing hybrid G-protein coupled receptors - mammalian DNA
producing hybrid G-protein coupled receptors - mammalian DNA
producing hybrid greceptors having at least one domain replaced
property sequences encoding receptor was constructed by replacing the DNA
cc sequence encoding the extracellular N-terminal domain with a DNA
cc sequence encoding the extracellular N-terminal domain of the
cc sequence encoding the extracellular N-terminal domain of the
cc saccharomyces cerevisiae STE2 gene product.
cc construct pHRS17 comprises this sequence together with a TPI1
cc construct pHRS17 comprises this sequence together with a TPI1
cc transcriptional promoter and terminator. The construct is used to
cc transform yeast cells. For the detection of the presence of a ligand in
cc a test sample, the culture of the yeast cells may be exposed to the test
cc sample, under conditions allowing binding of the receptor and ligand.
cc expensive and labour intensive then previous methods and does not
cc expensive and labour intensive then previous methods and does not
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22-AUG-1991.
08-FEB-1991;
08-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta2-adrenergic-STR2 hybrid receptor (1).
AR; adrenergic receptor; G-protein; ligand; screening; internal; extracellular; N-terminal; C-terminal; effector; domain; ss.
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Q13381;
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               Other examplary DNA sequences encoding hybrid G protein-coupled receptors are as follows: (1) the C-terminal internal effector domain is replaced; (2) the N-terminal extracellular and C-terminal internal effector domains are replaced; and (3) the N-terminal extracellular domain, the third internal effector domain and C-terminal extracellular domain, the third internal effector domain and C-terminal extracellular domain.
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protein-coupled receptor"
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KW asthmat
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Matches 19; Conser
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See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Claim 5; Page 23-26; 47pp; Japanese.
This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 125I-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1400 BP; 304 A; 402 C; 363 G; 328 T;
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24-MAR-1997;
27-MAR-1996;
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Beta-2 adrenalin receptor
Beta-2 adrenalin subtype;
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                                                                                                                                                                                Beta-2 adrenalin receptor subtype coding sequence. Beta-2 adrenalin subtype; cyanopindrol; agonist; asthmatic disease; ss.
                   W09735963-A1.
02-OCT-1997.
24-MAR-1997; J00982.
27-MAR-1996; JP-072914
                                                                                                                        Key
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/note= "xaa=Leu, Ile"
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Pred. No. 0.62;
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V304AC.

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                                                                                                                                                                                                                                                                                                                    Caning beta 2 and beta 3 adrenergic receptors and coding sequences - was full for identifying specific ligands and (ant)agonists to develop proper specific treatments for obesity in dogs of the canine beta 2-adrenergic constructed from polya+ RNA purified from dog brown adipose tissue cells. The sequence was a 600 bp fragment of the coding region of the human beta 3 cc constructed from polya+ RNA purified from dog brown adipose tissue cells. The probe was a 600 bp fragment of the coding region of the human beta-3 cc transmembrane domain 5 (TMS). The full length insert was cloned into M13 cc expressed e.g. in a mammalian cell, by subcloning into an expression vector such as pCDNA3. The beta-2 receptor can be used in comparative structure-function studies, e.g. for differential screening of ligands specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

So Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
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Best Local :
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02-OCT-1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
(VETI-) VETICEN.
Drumare MF, Lenzen G, Pietri-Rouxel F, WPI; 98-032136/03.
P-PSDB; W44932.
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This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine; beta-adrenergic receptor coding sequence.

Chybridisation; ligand; ss.

Canis familiani.
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V30468;
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19; Conserv
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PS Disclosure: Page 33-35; 46pp; English.
PS Disclosure: Page 33-35; 46pp; En
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
Homo sapiens.
WO9845437-A2.
15-OCT-1998.
10-APR-1998; U06956.
                                                                   EST clone DUG)5.

EST clone DUG)5.

Expressed sequence tag; secreted protein; haematopolesis regulator; Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h tissue growth; activin; inhibin; tumour inhibitor; ds.
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26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM) BRICHAM & WOMENS HOSPITAL.
Boushey H, Chinchilli VM, Drazen JM, Fish JE,
WARTIN RJ;
WPI; 98-506372/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patient; homozygous for allele encoding Arg at position 16 of
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polymorphism; ds.
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Human beta-2-adrenergic
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V52614;
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1633
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1588. .2829
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                                                                                                                                                                                                                             cDNA; 432
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               This sequence represents a partial human nucleotide sequence that codes for EZA binding protein (EZA-BP, see #36815). It was isolated from a human aortic expression library using the bHLH domain of E47 as probe. EZA-BP is expressed in vascular smooth muscle cells; mRNA is preferentially expressed in the aorta. EZA-BP interacts with EZA proteins in vivo, binds to both E12 and E47 and inhibits binding of E47 homodimer to an E-box probe (see T97606). A full-length DNA sequence is given in T97610, and mouse (see T97611) and rat (see T97612-13) EZA-BP sequences have also been isolated. EZA-BP nucleic acids may be used in gene therapy and antisense methods for treating vascular diseases such as afteriosclerosis, to produce transgenic or knock-out animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
Claim 1; Page 95; 641pp; English.

The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity,
                                                                                                                                                                                                                                                  inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or retinopathic diabetes
                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1996; US-013439.
(HARD ) HARVARD COLLEGE.
Endege WO, Haber E, Layne MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human E2A-binding protein genomic DNA (partial sequence). E2A-binding protein; E2A-BP; human; vascular smooth muscle cell; wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy.
Sequence
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                                                                                                                                                                                                                                                                                                                                     WPI; 97-470808/43.
P-PSDB; W36815.
                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity. The EST sequences are also stated to be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agostino MJ, Jacobs K, Lavallie Racie LA, Spaulding V, Treacy M; WPI; 99-070078/06.
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nes 18; Conserv
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                                                                                                                                                                                                                                        14; Page 47-51; 90pp; English.
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 methods of producing
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Pred. No. 3.
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E2A-BP polypeptides
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RESULT 10
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TD T97610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting or stimulating growth of vascular smooth muscle cells, predictions or reatment of rheumatoid arthritis or retinopathic diabetes

Pretinopathic diabetes

Claim 9; Page 55-60; 90pp; English.

Chis sequence represents a full-length nucleotide sequence that codes for human E2A binding protein (E2A-BP, see W35816). It was isolated from a human aortic RNA following 3 rounds of 5'RACE procedures. E2A-BP is expressed in vascular smooth muscle cells; mRNA is preferentially expressed in vascular smooth muscle cells; mRNA is proteins in vivo, binds to both E12 and E47 and inhibits binding of E47 homodimer to an E-box probe (see T97606). Mouse (see T97611) and rat (see T97612-13) E2A-BP sequences have also been isolated. E2A-BP nucleic acids may be used in gene therapy and antisense methods for treating vascular diseases such as arteriosclerosis, to produce transgenic or knock-out animals, as well as in methods of producing E2A-BP polypeptides that can be used therapeutically to promote vascular smooth muscle cell growth
                                                                                                                  Query Match
Best Local S
Matches 16
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Best Local
2626
                                                                                                                                                                                                                                                                e.g. for wound healing, or to screen for modulator compounds useful e.g. for the treatment of arteriosclerosis and anglogenesis. The E2A-BP gene promoter can be used in gene therapy methods to direct vascular smooth muscle cell-specific expression of the E2A-BP gene, antisense sequences or heterologous genes.

Sequence 3854 BP; 899 A; 1214 C; 1161 G; 580 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used therapeutically to promote vascular smooth muscle cell growth e.g. for wound healing, or to identify modulator compounds suitable for treatment of e.g. arteriosclerosis and angiogenesis. Sequence 2795 BP; 653 A; 828 C; 842 G; 472 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human and mouse E2A binding proteins - useful for inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human E2A-binding protein cDNA.
E2A-binding protein; E2A-BP; human; vascular smooth muscle cell; wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.
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Endege WO, Haber E, Layne
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27-MAR-1998
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14-MAR-1997; U04117.
15-MAR-1996; US-013439.
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TGACGATGCCCATGCC
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                                                                                                                  Score 16; DB; Pred. No. 23; 0; Mismatches
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23;
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RESULT Q43662 ID Q4

11

Q43662 standard; DNA; 4131 BP

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PP 14-OCT-1993; U08756.
PR 29-NOV-1991; US-800218.
PR 29-NOV-1991; US-800218.
PR (WEYE ) WEYERHAEUSER CO.
PI Ben-Bassat A, Benziman M, Calhoon RD, Gelfand DH;
PI Tal R, Wong HC;
DR PPSDB; R38155. R38156.
PP PSDB; R38155. R38156.
PT cyclic di:guanosine mono:phosphate degradation enzymes e.g.
PT cyclic di:guanosine mono:phosphate dispersor trange, mobilisable cosmid pNT2300S5. The average insert size was ca.
CC agene bank of Acetobacter 1306-11 was constructed in the broad host crange, mobilisable cosmid pNT230CS5. The average insert size was ca.
CC Golb. The bank was screened with a 53bp PCR amplified grobe whose cyclase encoding gene. Three unique cosmid classes were identified CC corresponding to three different cdg operons. The cdg3 operon comprises at least 2 genes. Manipulating the expression levels of che different cdg3 genes is contemplated, particularly in cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1993 (first entry)
Acetobacter cdg3 operon.
Cyclic diguanylate; diguanylate phosphodiesterase;
diguanylate cyclase; cellulose production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cde
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Key Loca
cds 387.
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13-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- dgc3
/note- "a diguanylate cyclase gene;
/note- "a diguanylate cyclase gene;
the ORF is described as continuing to
nucleotide 4143 although the sequence is
only shown up to nucleotide 4231. The ami
acid sequence R38156 cannot be deduced
directly from this open reading frame whi
is given as printed in the specification"
ce 3848. .3850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence"
741. .742
                                                                                                                                                                                                                                                                                                                                                                                                                              /codon= seq:GGG;
3962. .3963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 will restore 2522. .2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"a diguanylate phosphodiesterase gethe amino acid sequence R38155 cannot be deduced directly from this open reading frame due to a number of apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon= seq:CC; aa:Ala
/note= "insertion of G
2560 will restore the r
2657, .4131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon= seq:GG; aa: Trp
/note= "insertion of T between
/2522 will restore the reading i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon= seq: GT; as: Val
/note= "insertion of N betwee
743 will restore the reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frame due to a
(typographical
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387. .2606
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/label= pdeA3
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        864
                                                                                                                                                                                                                                                                                                                                                                                                seq:CC; aa:
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reading frame*
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eading frame"
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1197
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Query Match

81.18;

Score 15.4;

DΒ

1;

Length 4131;

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RESULT
Q31652
ID Q31670
AC Q3
AC Q3
AC Q3
AC Q3
AC Q3
AC Q4

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Q31655
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PS Claim 3; Page 25; 36pp; English.

CA clone encoding PR protein P14a (see Q31652) was isolated from a CC CDNA library established from infected tomato plants. The 11brary was screened for P14 genes using a probe (Q31657) based on CC the known P14 sequence (EMBO Journal, vol.4. #11, 2745-2749, 1985). The P14a clone was then used as a probe to screen a genomic library CC for other members of the P14 family. An overall total of 6 genes were identified, of which 5 are located in a 50kb stretch in the CC tomato genome, one of the genes appearing to be a pseudogene. The P14e protein is very similar to the P14a protein though has a CC stretch of 9 amino acids (residues 127 to 135) deleted from its CC-terminal and the last 2 C-terminal amino acids (residues 125 and C 126) substituted with respect to P14a. This gives a homology of 90% between the P14a and P14e mature proteins.

CS Sequence 453 BP; 110 A; 102 C; 119 G; 122 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local 9
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26-NOV-1992.
14-MAY-1992; I
15-MAY-1991; (
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1579 CATGACCATGCCCATGC 1595
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(SANO ) SANDOZ PATENT GMBH.
(SOHEN Y, Guegler K, Moesinger E, Niderman T;
COhen Y, Guegler K, Moesinger E, Niderman T;
P-PSDB; R28353.
P-P
                                                                                                                                                                            Pathogenesis-related protein P14a gup PR-protein; fungicide; rust fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogenesis-related PR-protein; fungicide
                                                                       signal_peptide
                                                                                                                                              Lycopersicon esculentum.
                                                                                                                                                                                                                                                       07-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                       Q31652 standard; cDNA; 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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GB-010544.
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/*tag= k
/*tag=
73..47
                                                                       Location/Qualifiers
1..72
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88.9%;
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                                                                                                                                                                        P14a gene isolated from fungus; powdery mildew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.8;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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for treating fungal infection of e.g. Uromyces appendiculatus, PT Erysiphe graminis, etc. in plants

PS Claim 3; Page 22; 36pp; English.

CC A cDNA library was established from infected tomato plants. The CC library was screened for P14 genes using a probe (Q31657) based on CC the known P14 sequence (EMBO Journal, vol.4. #11, 2745-2749, 1985).

CC A positive clone containing an ORF of 480bp was isolated and CC sequenced. It was found to encode P14a, a 159 amino acid protein CC differing from the previously published P14 protein by 5 additional CC maino acids (at AA positions 99-103, inclusive). The P14a cDNA was CC used to screen a genomic library for other members of the P14 CC family, P14a has fungicidal activity and can be used to combat rust CC see Q31652-Q31660.
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Best Local S
Matches 16
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26-MOV-1992; E01063.
14-MAY-1992; E010544.
15-MAY-1991; GB-010544.
(SANO) SANDOZ LTD.
(SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ PATENT GMBH.
COhen Y, Guegler K, Moesinger E
WPI; 92-415778,750.
                                                                                                                                          06-JAN-1994.
06-JAN-1993; U06228.
29-JUN-1993; U05-907138.
30-JUN-1992; US-940389.
03-SEP-1992; US-945173.
24-MAR-1993; US-05555.
24-MAR-1993; US-036555.
(CAMB-) CAMBRIDGE NEUROSCIENCE.
(CAMB-) LUDWIG INST CANCER RES.
CLUDW-) LUDWIG INST CANCER RES.
Chen MS, Goodearl A, Hiles I, Stroobant P, Waterfield M;
WPI; 94-025882/03.
wherein WYBAZCX is composed of the polypeptide sequences R55639-53 and R55766-75, wherein W comprises polypeptide segment F, or i wherein Y comprises polypeptide segment E, or i wherein Z comprises polypeptide segment G, or i
                                                                               Glial mitogenic polypeptide factors glial cell mitogenesis and treating glial cell Fig 31: 178pp; English. The DNA sequence encoding a polypept
                                                                                                                                                                                                                                                                                                                                                    GGF gene coding segment I.
Glial growth factor; GGF; heregulin; mitogenesis;
Schwann cell; tumour; central nervous system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Q66939
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                   P-PSDB; R55774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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C/D C/D' H, C/D C/D' D, C/D D' HL, C/D D' HKL,
C/D C/D' D' H, C/D C/D' D' HK, C/D C/D' D' HL,
C/D C/D' D' HKL, C/D C/D' D' H, C/D C/D' D' HL,
C/D C/D' D' HKL, or C/D' D' HL;
C/D C/D' D' HKL, or C/D D' HL;
C/D C/D' D' HKL, or C/D D' HL;
C/D C/D' D' HKL, or C/D D' HL;
C/D C/D C/D' D' HKL, C/D C/D' D, C/D D' HKL,
C/D C/D HKL, C/D C/D' HKL, C/D C/D' D' HKL,
C/D C/D' HKL, C/D C/D' D' HKL, C/D C/D' D' H, C/D
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C/D D' HL, C/D C/D' D' HKL, C/D C/D' D' H, Or C/D
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Best Local S
                             Matches
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17-FEB-1994.
10-AUG-1993; US-927337.
10-AUG-1992; US-927737.
25-SEP-1992; US-951747.
01-DEC-1992; US-94085.
29-JAN-1993; US-011396.
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Glial ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGF gene coding segment L. Glial growth factor; GGF; heregulin; proliferation; antibody; Schwann cell; tumour; central nervous system; inhibition;
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GGF gene codi
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Claim 6-7, 21-24; Fig 31; 178pp;
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Gwynne DI, Marchionni M, McBurney
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VYBAZWX
polypeptides comprising FBA, FBA segments are used for inhibiting
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    Issued_Patents_NA:*

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2: /cgn2_6/ptodata/1

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/cgn2_6/ptodata/1/lna/5D_COMB.seq:*
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GENERAL INFORMATION:
APPLICANT: Sledziewski, Andrzej Z
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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LENGTH: 191 base pairs
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                    COMPUTER READABLE FORM:
                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                             APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: ...
STREET: Seattle
                                COUNTRY: United
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100. nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: POFILING DATE: 19910208
CLASSIFICATION: 435
                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: United States 98104-7092
                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3723836
                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                   E: Seed and Berry
6300 Columbia Center, 701 Fifth Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Columbia Center, 701 Fifth Ave
                                                   United States
                                                                                                                                                                                                                   Sledziewski, Andrzej Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheppard, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sledziewski, Andrzej Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seed and Berry
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Protein-Coupled Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 6
Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                           PILING DATA: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PATE: 29-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Tal, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 99
                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACATGACGATGCCCATGCC 103
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LOCATION:
                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                STREET: 2730 Sand
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 200 C. ... 206-682-6031
REFERENCE/DOCKET NUMBER:
               REGISTRATION NUMBER:
                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                  94025
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           Bortner, Scott R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08309512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1242 base pairs
                                                                                                                                                                                                                                                                               2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                   wong,
                                                                                                                                                                                                                                                                                                                                                              Calhoon, Roger D.
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Gelfand, David H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                              Ben-Bassat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                      CYCLIC DIGUANYLATE METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                          63
                                                                    US 07/800,218
                                                                                                                         us/08/309,512
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8145-008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1242;
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Gaps

TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 854-3660

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                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION NUMBER: PCT/US92/08756A
FILING DATE: 1921014
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
AP
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                                                                         TELEX: 278356 INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1579 CATGACCATGCCCATGC 1595
                                                                                                                                                                            NAME: BOTTNEY, SCOTT R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: WENTELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
NUMBER OF SEQUENCES: 11
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APPLICANT:
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APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: CA
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2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
                                                                                                                                           415-433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tal, Ronny
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94.1%; Pred. No. 4
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                                                                                                                                                                                                                                                      WEYR 20050 USA
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HYPOTHETICAL: NO
ANYI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Acetobacter xylinum
PCT-US92-08756A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                         TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1579 CATGACCATGCCCATGC 1595
                                                                                                                              APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: T9a1, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 5250.4
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION NUMBER: 07/940,389
PRITTY NUMBER: 07/940,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM.TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
                     SEQUENCE CHARACTERISTICS:
LENGTH: 730
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York City
STATE: New York
                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 catgacgatgcccatgc 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7, Application US/08036555B 5530109
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felfe & Lynch
                                                                                             (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/036,555B
24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 5.25 inch,
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                                                                                           688-9200
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 kb storage
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US-08-036-555B-77

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; TOPOLOGY:
US-08-469-569-77
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                     TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Minghetti
APPLICANT: Chen, Mai
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
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                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                    STRANDEDNESS:
                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 10-APR
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 30-JUI
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 03-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 catgacgatgcccatgcc 19
                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                  TELEPHONE:
                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08469569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minghetti, Luisa; Waterfield, Michael; I
Chen, Maio Su; Hiles, Ian
WENTION: Glial Mitogenic Factors, Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodearl, Andrew; Stroobant, Paul;
Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
                   linear
                                                                                                                                    (212)
                                                                                                                                                                                                    Christine H.
                                                                                                                                                                                                                                    UMBER: U.K. 91 07566.3
10-APRIL-1991
                                                                                                                                                                                                                                                                                                                                                                                        UMBER: 07/940,389
03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                         UMBER: 07/907,138
30-JUN-1992
                                                                                                                                                                                                                                                                                     03-APRIL-1992
                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation and Use
                                                                                                                                    688-9200
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88.9%;
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                                                                                                                                                                     LUD 5250.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Query Match

77.9%;

Score 14.8;

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Length 730;

Mismatches

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Indels

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Gaps

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US-08-249-322A-77
                                                                                     US-08-249-322A-77
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Query Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 9
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
                                                                                                                                                                      TELEFAX: (212) 638-3884
INFORMATION FOR SFQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/96
FILING DATE: 23-0CT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-MAY-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-JU
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/863,703 FILING DATE: 03-APRIL-1992
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10022
                                                                                                                                     nucleic acid
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minghetti, Luisa; Waterfield, Michael; Marchioni, Wark;
                                                                                                         linear
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                                                                                                                                                                                                                                (212)
                                                                                                                                                                                                                                                                                                                                      UMBER: U.K. 91 07566.3
10-APRIL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1992
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                                                                                                                      single
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                                                                                                                                                                                                                                688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               07/907,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07/965,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                  Score 14.8;
Pred. No. 80;
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                                    DB 2;
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                                      Length 730;
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106 CATGACGGTGTCCATGCC 123

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; OTHER INFORMATION:
US-08-469-526A-77
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SOFTMARE: FASESEO for Windows Version 2.0
SOFTMARE: FASESEO for Windows Version 2.0
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,526A
FILING DATE: 06 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24 MAR-1993
FILING DATE: 24 MAR-1993
FILING DATE: 7/965,173
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
APPLICATION NUMBER: 07/965,173
APPLICATION NUMBER: 07/940,389
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-SUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: U.K. 91 0756
FILING DATE: 10-APRIL-1991
APPLICATION NUMBER: 07/863/0756
FILING DATE: 11-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BLEKET-BEADY, KI1Sting
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/0
TELEPHONE: 617-428-7045
TELEPHONE: 617-428-7045
TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7. Patent No.
                                                                                         Query Match
                                                       Matches
                                                                                                                                                                                                                                                                    TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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106 CATGACGGTGTCCATGCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
                                                                Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110
                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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2 catgacgatgcccatgcc 19
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176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minghetti, Luisa
Waterfield, Michael
Marchionni, Mark
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                                                       Conservative
                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                   04585/00200A
                                                     0,
                                                                      Score 14.8;
Pred. No. 80
                                                       M1smatches
                                                                                         DΒ
                                                                                       <u>ν</u>
                                                     <u>ي</u>
                                                                                     Length 730;
                                                     Indels
                                                     0;
                                                     Gaps
                                                     0
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US-08-734-591A-77
; FEATURE:
; OTHER INFORMATION:
US-08-734-591A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION 22-OCT-122.
FILING DATE: 22-OCT-122.
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,335
APPLICATION NUMBER: 06-JUN-1995
                                                                                                                                                                                  PRIOR APPLICATION DATA: 10.2

APPLICATION NUMBER: UK 91 07566.3

FILING DATE: 10-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109

REGISTRATION NUMBER: 04585/00200P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 428-0200

TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/03
APPLICATION NUMBER: 08/03
APPLICATION NUMBER: 08/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: WordPerfect (Version 7.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-MAR-1993
PAPPLICATION DATA:
PAPPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                   TOPOLOGY:
                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7, Application US/08734591A 5854220
                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stroobant, Paul
Minghetti, Luisa
Waterfield, Michael
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                                                     linear
                                                                                                                                                                                                                                                                                                                                                                               NUMBER: 07/863,703
03-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WUMBER: 07/940,389
03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/734,591A
22-OCT-1996
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                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/036,555
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Query Match

Local

Similarity

77.9%; 88.9%;

Score 14.8; Pred. No. 80

DB

3;

Length 730;

0;

Gaps

0;

PCT-US94-05083C-178

Mismatches

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US-08-469-660-182
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:.
APPLICATION NUMBER: 08/011,396
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/984,085
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
APPLICATION NUMBER: 07/951,747
                                                                                                                                                                                                                                                               TELEFAX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gwynne, David I.; Marchionni, Mark; APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION, TITLE OF INVENTION: THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                               NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/017004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: 07/92
FILING DATE: 10-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
ZIP: 0211-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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106 CATGACGGTGTCCATGCC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/469,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                       Local
                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                              LENGTH:
                           2 catgacgatgcccatgcc 19
                                                                     16;
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                                                                                       Similarity
                                                                                                                                                                                                           nucleic acid
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225 Franklin Street
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                                                                      Conservative
                                                                                                                                                                             linear
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                                                                                                                                                                                          double
                                                                                       77.98;
                                                                                                                                                                                                                                                                                                                                                                                                                            07/927,337
                                                                        0;
                                                                                       Score 14.8;
Pred. No. 8
                                                                      ed. No. 80;
Mismatches
                                                                                                          DB 3;
                                                                                                          Length 730;
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                                                                          Gaps
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RESULT 12

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                                                                                                                                                                                                                             Sequence 77, Application PC/TUS9506846A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS FOR ALTERING TITLE OF INVENTION: MUSCLE CONDITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Robert Sklar, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                    APPLICANT: Goodearl, Andrew David; Stroobant, Paul; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; APPLICANT: Chen, Maio Su; Hiles, Ian TITLE OF INVENTION: Glial Mitogenic Factors, Their TITLE OF INVENTION: Preparation and Use NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                          106 CATGACGGTGTCCATGCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PC FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, !
MEDIUM TYPE: kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
                          ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                              2 catgacgatgcccatgcc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
16; Conserv
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10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-8906
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                 USA
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 80;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette,

5.25 inch,

360 kb storage

OPERATING SYSTEM:

PC-DOS

Wordperfect

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RESULT 14
US-07-640-476-6
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: SCHUURHUIZEN, PAUL 1
APPLICANT: MRABET, NADIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/036,555
FILING DATE: 24 MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION UMBER: 07/940,389
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PCT/US95/06846A
                                                              TITLE OF INVENTION: NOVEL GLUCOSE
TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTILION & FOETSTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HANBON, NOTMAN D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-APRIL-19:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/863, FILING DATE: 03-APRIL-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: U.K. 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,322
FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                      106 CATGACGGTGTCCATGCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                  CITY:
                                                   STREET:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         2 catgacgatgcccatgcc 19
                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                         n 77.9%;
Similarity 88.9%;
              Menlo Park
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                   545
                                                                                                                                                                      SCHUURHUIZEN, PAUL W.
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                               Morrison & Foerster
15 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: U.K. 91 07566.3
10-APRIL-1991
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                                                                                                                                       ISOMERASE
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Query Match
Best Local Similarity
"atches 16; Conserve
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                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Productive of INVENTION: Heregulin
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/07847743B Patent No. 5367060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11near MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDJUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
OTHER INFORMATION: /EC.
OTHER INFORMATION: /prc
OTHER INFORMATION: /ev/
OTHER INFORMATION: /st/
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LENGTH: 1164 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
                                                                                                                                                                                                                                                                                                                                                                                                                                     249 CATGACGGTGCCCATGGC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces murinus STRAIN: DSM 40091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kate H. Murashige REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: 19910110
                                                                                                                      COUNTRY:
                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1...
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88.9%;
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[7] conumber = 5.3.1.5
[7] /product = "xylose isomerase (glucose isomerase)"
[7] /evidence = EXPERIMENTAL
[7] /standard_name = "D-xylose ketol isomerase"
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APPLICATION NOMERS: US/07/847,743B

PILING DATE: US/00/86

PRICES APPLICATION DATA:
APPLICATION NUMBER: 07/705256

PILING DATE: 24-by-1951

PILING
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
September 12, 2000, 22:46:44; Search time 1893.64 Seconds (without alignments) 44.246 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est49:*
gb_est41:*
gb_est42:*
gb_est42:*
gb_est44:*

gb_est35: gb_est36: gb_est37: gb_est38: em_est27: em_est28:

em_est22: em_est23: em_est24: em_est25: em_est26: em_est26: gb_est33: gb_est34:

gb_est25:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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16.
C18250 377 bp mRNA EST 02-CCT-1996 C18250 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-559E06 5', mRNA sequence.
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121:
122:
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AJ272869
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AV147821
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AA666234 HS_539_B
AA603161 np55e04.s
AL026701 Fugu rubr
AU064622 AU064622
AU558009 fc89e11.y
AW421540 fj92f07.y
AW421540 fj92f07.y
AW421540 fj92f07.y
AW421541 fj82f07.9
AW421541 fj82f07.9
AW421541 fj82f07.9
AW421541 fj84f11.y
AU667783 HS_203_B
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AQ127481 mh49h11.r
                                                                                                                                      AJ272869 AJ272869
AV391075 AV391075
AQ937984 NB6-748R
AQ413101 RPCI-11-1
AQ050823 nbxb0004c
                                                                                                                                                                                                                                                                                                       AL122275 Fugu rubr
AW134110 fil6d03 y
AW34338 fi16h11 y
AA246435 LD05332.5
AW343362 fi76f07 y
AL065380 Drosophil
AA495310 fa01a12.r
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D21603 MUS73A02 mo
AL047823 DKFZp586G
AW580751 PM3-LT003
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AI870022 w163h10.x
AQ681306 HS_5488_B
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R35420 yg65e10.rl
AW351478 RC1-BT00
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AI444193 fb44g04.y
AQ942891 Sheared D
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AUTHORS
TITLE
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AI870022/c
LOCUS
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JOURNAL
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Best Local
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C18250.1
                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                   A1870022 522 bp mRNA EST 07-MAR-2000 w163h10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:242963 similar to SW:NPI2_MOUSE P51860 NUCLEOSOME ASSEMBLY PROTEIN 1-2; contains element MER22 repetitive element; mRNA sequence. A1870022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuka cDNA project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                          (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
On Jan 19, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tsutomu Fujiwara
               CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                Bonaldo,
                                                                                                                    Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                               cDNA Library Preparation: M. Bento Soares, wonaldo, Ph.D.
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       o.llnĬ.gov/bbrp/image/image.html
Length: 820 Std Error: 0.00
                                                                                                                                 Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="GEN-559E06"
/clone_lib="Human placenta.cDNA (TFujiwara)"
/tissue_type="placenta"
/113 c 101 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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Pred. No. 15;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                              sapiens cDNA clone IMAGE:2429635 3'
                                                                                                                      M.D., Myrna R.
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                                                                                                                                                                    replaced gi:2286321.
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                                                                  High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pletcr@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1064 row: N column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ681306 556 bp DNA GSS 25-JUN-1999
HS_5488_B1_G03_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1064 Col=5 Row=N, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ681306.1
GSS.
                   High quality sequence stop: 556
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             On Mar 23, 1999 this sequence version Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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157 c 94 g 174 t 1 others
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/clone="IMAGE:2429635"
/clone_11b="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ity sequence stop:
Location/Qualifiers
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94.7%;
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Adams, M.D.
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JOURNAL COMMENT
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AUTHORS
TITLE
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AW424650/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
On Oct 6, 1998 thi
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea. 1 (bases 1 to 612)
                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 707020 row: G col
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
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707020G08.x1 707 - Mi
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                 Similarity
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                                                                                             /note-*Organ: tassel, kernel, silk, husk, root, leaf; vector: pGADJ0; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned.*

a 171 c 185 g 108 t
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                                                                                                                                                                                                                                                     (SK)"
                                                                                                                                                                                                                                                               /db_xref="taxon:4577"
/clone_lib="707 - Mixe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1064 Col=5 Row=N"
                                                                                                                                                                                                   /lab_host-"DH10B"
                                                                                                                                                                                                             /tissue_type="tassel, kernel, silk, husk,
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                      /cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                   ∕organism-"Zea mays"
                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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               86.38;
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94.4%;
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Pred. No. 2.
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 Mismatches
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               16.4; DB
No. 3e+02;
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                                  612;
 <u>.</u>.
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On May 11, 1999 this sequence version replaced gi:4776626.
Contact: Takashi Aoki
Genetics and Biochemistry
Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C82152 800 bp mRNA C82152 Leukocyte of Japanese clone WH11-3, mRNA sequence.
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17; Conserv
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                                                   paralichthys olivaceus.

Paralichthys olivaceus.

Paralichthys olivaceus.

Paralichthys olivaceus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;

Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;

Holacanthopterygii; Acanthopterygii; Percomorpha;

Pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.

1 (bases 1 to 940)
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A survey of expressed genes in the leukocyte of Japanese flounder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paralichthys olivaceus.
Paralichthys olivaceus
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                                                                                                                                                                                                                             clone WD3-5, mRNA sequence.
C82248
C82248.1 GI:5039484
                                                                                                                                                                                                                                                                                       C82248 Leukocyte of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ad95217@s4201.tokyo-u-fish.ac.jp
clone WH11-3: similar to human KIAA0174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Paralychthys olivaceus) infected with Hirame rhabdo virus
(Paralychthys olivaceus)
                                 Nam, B., Katagiri, T.,
               survey of expressed genes in the leukocyte of Japanese flounder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Paralichthys olivaceus"
/db_xref="taxon:8255"
/clone="WH11-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="leukocyte infected with Hirame 221 c 194 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Leukocyte of Japanese flounder i"
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Pred. No. 3.1e+02;
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                                   Hirono, I. and Aoki, T.
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Contact: Takashi A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics and Biochemistry
Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japa
Tel: 03-5463-0556
                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 1655
High quality sequence stops: 153 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1655 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
On Dec 20, 1995 this sequence version replaced gi:1133491.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 214)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsonskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R35420 214 bp mRNA E y965e10.r1 Soares infant brain lNIB Homo IMAGE:38075 5', mRNA sequence.
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 03-5463-0690
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/db_xref="taxon:8255"
/clone="WD3-5"
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258 c 211 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                  /clone_lib="Soares infant brain
/sex="female"
                                                     /db_xref="taxon:9606"
/clone="IMAGE:38075"
                                                                                     /organism="Homo sapiens"
/db_xref="GDB:410616"
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/dev_stage="73 days post natal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5407415.
Contact: Simpson A.J.G.
Laboratory Cancer Genetics
Ludwig Institute for Cancer Research
Russ Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                              Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1st2=RC1-BT0077-
15099-001-H05&t3-1999-09-15&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 266.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   /note-*Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PGR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 7

a 80 c 93 g 57 t
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/db_xref="taxon:9606"
/clone_lib="BT0077"
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hes 0;
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis
                                                                                 (bases 1 to 463)

Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiems
EST (Koehrer, et al.)
Unpublished (1999)
On Jan 19, 1998 this sequence version replaced gi:2285034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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1 (bases 1 to 281)
Nishiguchi,S., Joh,T., Horie,K., Zou,Z., Yasunaga,T. and Shimada,K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells; characterization of low-abundance mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Apr 7, 1998 this sequence version replaced gi:3036588.
Contact: Kazunori Shimada
Department of Medical Genetics, Division of Molecular Blomedicine
Research Institute of Microbial Diseases, Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="73A02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib-"mouse embryonal carcinoma cell line 74 c 57 g 69 t 17 others
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Pred. No. 4.2e+02;
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                                                                                                                                      Gassenhuber, J. and Wiemann, S.
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Analysis, German Cancer
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AW580751/c
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                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl-PM3&t2-PM3-LT0031-
100100-003-d04&t3=2000-01-10&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
16; Conser
                                                                                                                                                                                                                                                        High
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Pr
Unpublished (1999)
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PM3-LT0031-100100-003-d04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKFZp586G0622) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jan 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
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                                                                                                                                                                                                                                                     quality
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                 /note="Organ: leiomios; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKF7p586G622"
/clone_lib="586 (synonym:
/tissue_type="uterus"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
159 c 132 g 73 t ·
                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
                                                                                                                          /dev_stage="Adult"
                                                                                                                                              /clone_lib="LT0031"
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                                                                                                                                                                                                                                  ocation/Qualifiers
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cDNA amplification
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similar to
AA595338
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Location/Qualifiers
                                                       l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1453 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 582)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Emmert-Buck, M.D., Ph.D.
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                                                       Conservative
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1 169 c 174 g 98 t
                                                                                                                                                                                                                                                                                                      /db_xref="taxon
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/db_xref="taxon:9606"
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                                                                  84.2%; Score 16;
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hes 0;
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                                                                              AA603161 335 bp mRNA
np55e04.el NCI_CGAP_Brl.1 Homo sapiens c
similar to gb:D21261 SM22-ALPHA HOMOLOG
AA603161
                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pleter de Jong (pletcr@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h GenetLes (lnfo@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 935 row: J column: 1 Seg primer: 77 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7cl: (206) 616-3618
7ax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Dec 15, 1999 this sequence version replaced gi:4575425 Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 649) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Koller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
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Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conser
                    1 (bases 1 to 341)
Elgar,G., Clark,M., Smith,S.,
Williams,G. and Brenner,S.
Direct Submission
                                                                                                    Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil; Perr
Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Fugu.
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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1 (bases 1 to 335)
1 (bases 1 to 335)
1 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                           GSS; genome sur
Fugu rubripes.
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Fugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                        AL026701.1 GI:3264044
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/clone_lib="NCI_CGAP_Br1.1"
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/db_xref="taxon:9606"
(09-JUN-1998) MRC Human Genome Mapping Project Resource
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Pred. No. 5.4e+02;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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GenEmbl:*
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gb_htg36:* gb_htg27:* gb_htg27:* gb_htg28:* gb_htg29:* gb_htg30:* gb_htg31:* gb_htg31:* gb_htg31:*	gb_htg3: * em_htg2: * em_htg2: * em_htg2: * em_htg3: * em_htg3: * em_htg3: * gb_p13: * gb_htg8: * gb_htg8: * gb_htg12: * gb_htg12: * gb_htg16: * gb_htg17: * gb_htg17: * gb_htg17: * gb_htg17: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c c 22 20 24	16 17 18	10 11 13 14	0 0 44207	Result No.
14 14 14	144	15 15 14.6 14	1	Score
93.33.3	93.393	100.0 100.0 100.0 97.3 93.3		Query Match
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I08083 I09103 E01676 HASMT HSU230B10	E07891 AF172121 CGU62588 HSL81779	ACO23555 ACO23555 CEY17G7 AL162574 AF202305 BACIS2401 BACIS2402	AF022954 AF022955 AF022956 HSBAR HUMADRBR CEY38G4 CEY17G7B AC004103	ID
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                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens beta2-adrenergic receptor (ADRB2) gene, AF022954
AF022954.1 GI:2570528
                                                                                                                                                                                 3 (bases 1 to 1242)
Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert
                                                                                                                                                                                                                                                                                         Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993) 93192047
                                                                                                                                                                                                                                                                                                          Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic in normal and asthmatic subjects
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases_1 to 1242)
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                                                                                                                         Erratum:[[published erratum appears in Biochemistry 1994 Nov 29;33(47):14368]]
4 (bases 1 to 1242)
Liggett, S.B. and Green, S.A.
                                                                                                                                                                  94347707
                                                                                                                                                                          Biochemistry 33 (32), 9414-9419 (1994)
                                                                                               Submitted (04-SEP-1997) Medicine, Ave ML670564, Cincinnati, OH 4526
                                                                                                                   Direct Submission
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                                                                                      Location/Qualifiers
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45267-0564, USA
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| 12 CAATAGAAGCCATGC 56
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Green,S.A., Turki,J., Innis,M. and Liggett,S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
94347707
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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S. B.
Reihsaus, in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects
Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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Liggett, S.B. and Green, S.A.
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/db_xref="G1:2570529"
/translation="MGQPGNGSAFLLAPNRSHAPDHDYTQERDEVWYVGMGIVMSLIV
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NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSILTKNKARVIILMVWIV
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYPDLVIMVFV
YSRVFQEAKRQLQKIDKSEGRRHYQNLSQVEDDGRTCHGLRASSKFCLKEHKALKTLG
IIMGTFTLCWLDFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor properties of the receptor J. Biol. Chem. 268 (31), 23116-23121 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green, S.A., Turki, J., Innis, M. and Liggett, S.B. Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propering the state of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propering the state of the state of
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1 (bases 1 to 1242)

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                                                                                                                                                                              Submitted (04-SEP-1997) Medicine, Univ of Ci-
Ave ML670564, Cincinnati, OH 45267-0564, USA
Location/Qualifiers
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Liggett, S.B. and Green, S.A.
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29;33(47):14368]}
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LAIVFGNVLVITAIAKERLQTVTNYFITSLACADLVMGLAVVEPGAAHILMKMTFG
NFWCEEWTSLDVLCVTASIETLCVIAVDRYFALTSPFKYQSLLTKNKARVILILAVUFV
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
YSRVFQBAKRQLOKIDKSEGRFHVQNLSQVEQDGFTGHGLRSSKFCLKEHKALKTLG
INMGTFTLCMLPFFIVNLTAKEVQNLTRKEVYTLLNWHGVYNSGFNPLLYCRSPDFTI
INFGTFTLCMLPFFIVNLTRKEVTLAFKTUR
INFGTFTLCMLPFTVANGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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/db_xref="GI:2570531"
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VERSION KEYWORDS

FEATURES

Sg

/note="N-linked glycosylation site"

TITLE

RESULT AF022956

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misc_feature
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1 (bases 1 to 2305)
Schofield, P.R., Rhee, L.M. and Peralta, E.G.
Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y00106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (20-OCT-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSBAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene for beta-adrenergic receptor (beta-2 subtype).
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IIMGTFTLCWLPFFIVNIYHYIQDNLIRKEYYILLMWIGYYNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHYEQEKENKLLCEDLPGTEDFYGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mgopgngsafllapnrshapdhdytoordeywygmgiymsliy
LAIVFGNYLVITAIAKFERLQTYTNYFITSLACADLYMGLAVVPFGAAHILMKMWTFG
NFWCEFWTSIDVLCYTASIETLCYIAVDRYFAITSPFKYOSLTKNKARVIILMYMIV
SGLISFLPIOMHWYRATHQEAINCYAMETCCDFFTNOAYAIASSIVSFYVPLVIMVFV
                                                                                                                                                  /translation="MGOPGNGSAFILAPNRSHAPDHDVTOORDEVWVVGMGIVMSLIV
LAIVEGNVLVITAIAKFERLOTVTNYEITSLACADLVMGLAVVPFGAAHILMKMMTFG
NFWCEFWTSIDVLCVTASIETICVIAVDRYFAITSPFKYGSKLTKNKARPKILLMVMFV
SGLTSFLPIOMHWYRATHOEAINCYANETCCDFFTNOAYAIASSIVSFYVPLVIMVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ADRB2"
/note="Thr164 to Ile polymorphism"
/replace="c"
330 c 325 g 311 t
                                                     TVPSDNIDSQGRNCSTNDSLL"
                                                                          YSRYFQEAKROLQKIDKSEGRFHYONLSOVEODGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVIODNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEOSGYHVEOEKENKLLCEDLPGTEDFVGHOG
                                                                                                                                                                                                                                                          /protein_id="CAA68289.1"
/db_xref="GI:29371"
/db_xref="SWISS-PROT:P07550"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Maniatis human"
/clone="lambdahbetaAR17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="AABB2151.1"
/db_xref="GI:2570533"
                                                                                                                                                                                                                                                                                                                                  /note="beta-adrenergic receptor (AA 1 - 413)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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'note="N-linked glycosylation site"
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87222338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)

Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,
Dixon,R.A., Keller,P., Caron,M.G. and Lefkowitz,R.J.

Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenergic receptor. Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta-2-adrenergic M15169 J02728 M16106
                                                                                                                                                                                                                                                                           cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor platelet-derived growth factor Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M15169.1 GI:178201
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Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions
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/note="membrane s
1247. .1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="membrane spanning domain VII"
/note="membrane spanning domain VII"
/note="membrane spanning domain VII"
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1616. .1687
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/note="membrane spanning
1007. .1078
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                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="b-2-adr mRNA (alt.);
                                                                1369
                                                                              /gene="ADRB2"
/note="b-2-adr mRNA (alt.);
                                                                                                                1369.
                                                                                                                                                            tissue_type="placenta"
                                                                                                                                                                           'clone="pTF."
               'gene="ADRB2"
                                                                                                                           map="5q31-q32"
                                                                                                                                              tissue_lib="Evan Sadler"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3451 bp
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G00-120-541"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans chromosome II clone Y38G4, PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                              jes@sanger.ac.uk or rw@nematode.wustl.edu
On Oct 7, 1997 this sequence version replaced g1:2464982.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
of segments is not known; 800 n's separate segments.

* NOTE: This is a 'working draft' sequence

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-OCT-1997) Nematode Sequencing Project, Sanger Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z99713.1 GI:2467102
HTG; HTGS_PHASE1.
                                                                                                                        with foreign sequence from E.coli, yeast, vector, phage etc. Order
                                                                                                                                                                  contaminated
                                                                                                                                                                                                  the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulston, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditina; Rhabditolue 1 (bases 1 to 117864)
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                                                                                                                                                                                              sequence may change as work continues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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//db_xref="GDB:G00-120-541"
//db_xref="GDB:G00-120-541"
//product="beta-2 adrenergic receptor"
/protein_id="AAA88015.1"
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                                                                                                                                                                                                       http://wcbacc.sanger.ac.uk/cgi-
bin/display?db-wormace&class-Sequence &object=Y17G7B
bin/display?db-wormace&class-Sequence &object=Y17G7B
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note entire insert of
the Specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission

Submitted (09-JUN-1998) Nematode Sequencing Project, Sanger Centre, Submitted (09-JUN-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Williams (1998) Nematode United Sequencing Project, Sanger Centre, Washington University, St. Louis, WO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode C. elegans:
Investigating biology. The C. elegans Sequen
Science 282 (5396), 2012-2018 (1998)
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                                                                     neighbouring submissions.

The true right end of clone W03C9 is at 100 in this sequence. The true right end of clone Y17G7 is at 143092 in this sequence. The start of this sequence (1. 100) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erratum: [[published errata appear in Science 1999 Jan
1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
3;285(5433):1493]]
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end of this sequence (142993. .143092) overlaps with the start
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/chromosome="II"
/clone="Y38G4"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  egans: a platform for 
Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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14218. .14331,14622. .14673,18228. .18428,18624. .18714,
19438. .19658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKKYHFGGFKQGDVLGCLIHLPVDKKLQIPANLPSEKYLPVSHKGFNLISFKANYFFE
VQEESADIAKTLVEMPGSYIEFFHNGKSCGKAYENIYAGAYYPSISIFKSATATMNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVSKGTWYFEVNFDDQPDDSHIRIGWSQSYASLQACVGYNKFSYGWRSKHGTKFHEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRGASKRRHAEAPYTGKKOKLAADYSSTAAPNGVQIDIPFSKDNYRYYLTEVDPNVPE
DPAWNONOSSAYVIPSFHYRELLNPTVNVSSNDRAFOLSINGNSITGFEGYSMARASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERLKADGKLSAEHVPEDFTYLSLKDETVPYMNENWYMLTATKQKKEWHQNLAPTLLKE
KNIFVQHNDDDDLFALAEKNLSLLGPLHEAVKLIGKRPTERENREPRHTELPPTEGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11683. .19658
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18624. .18714,19438. .19658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:Q9XXJ2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(3569. .3750,3804. .3945,4851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3569. .4874)
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                                                                                                                                                                                                                                                                                                                                         ATMNLGPK FRNLPRGATG I HARADEQQHEQTLSDMLYLVSKEVNLDHPPRVKREDDDD
                                                                                                                                                                                                                                                                                                                                                                    IFPIFLAFSLFYIEIFQGDVLGCLIHLPVDKKLQIPANLPSEKYLPVSHKGFNLISFK
ANYFFEVQEESADIAKTLVEMPGSYIEFFHNGKSCGKAYENIYAGAYYPSISIFKSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKFRNLPRGATGIHARADEQQHEQTLSDMLYLVSKEVNLDHPPRVKREDDDDVKDIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGRCLKEFHEFSRNSNGVPFMICYTFTCKQCRPTAEDWKAKKADLVQMCVTVLATLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q9XXH4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Y17G7B.2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Y17G7B.2c"
11683. .19658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Y17G7B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Caenorhabditis elegans"
/db_xref-"taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="cDNA EST EMBL:D35727 comes from this gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to Acyl CoA binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L. .14309
                                                                                                               'note="Y17G7B.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="Y17G7B.2c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="GI:3947596"
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CDS

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EESADIAKTLVEMPGSYIEFFHNGKSCGKAYENIYAGAYYPSISIFKSATATMNLGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASKRRHAEAFVTGKKOKLAADYSSTAAPNGVOIDIPFSKDNYRYYLTEVDPNVPEDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mrsskggrgrqaapktapttvcycdgkrelgsvevvcstclkwf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="myyvksllrradnemyivkkssearaallvdlyneedykeladk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="X17G7B.3"
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TBPILSREDVLCVIRDSVDSVEDERLAKFVVGNHRTHHEDAKKIVKEGDELEEDQMDE
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to MCM2/3/5 family; cDNA EST EMBL:T02370 comes from this gene; cDNA EST yk244e4.5 comes from this gene; cDNA EST yk40748.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(32881. .37816)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAVKSFKTGSTILGGGVVKHHINNANLMRNGADHTVYINTGQEFDGSDSGAQPDEAVS
WGKVKPSAGAVKVHAEATLVFFLLVAETFAKHEGHKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDFSLSAILSSYMSTGFQATHLAQAIQOVNQMLSLRDTPLTCDDDEKLFPYPEGRQKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Y17G7B.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA19450.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(32881. .33253,34402. .35645,36629. .37493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Y17G7B.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to Metallo-beta-lactamase superfamily"
                                                                                                                                                                                                                                                                                                                                               DEAVAKEIERRFKNFLRSFHEPGNKQTKYIQMIKSMAADNRESLEVSFTDLSDDNGEQ
                                                                                                                                                                                                                                                                                                                                                                                        ALMY EDGDS EEVDT RRRGRGRRGRGDAADDDSVPMEEEDI PVDI LENI RGRT I RDHVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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VESMIRLSEAHAKLHLRSYVNDEDCAAAIRVMLESFVNTQKASIMRMMKKTFSRHLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA19452.1"
/db_xref="GI:3947600"
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                                 RTGVRLIPQDLLRKYIIYAREKCHPTLPEQHSEKFSNIFAQMRKESMATGSVAITVRH
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cdsgene

gene

FEATURES

Exon/Intron boundaries of identified were canonical splice junctions that across the splice junctions.

genes were maintained

chosen if there sequence continuity

Location/Qualifiers /organism="Homo sapiens"

.144368

Sequence similarities were identified using Powerblast by Jinghui

The repeat regions shown were identified using RepeatMasker by

source

CDS

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VERSION
KEYWORDS
SOURCE
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Carvelli,K., Chacko,J., Chen,J., Di,W., Ding,Y., Dugan,S.,
Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M.,
Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S.,
Kampal,R., Karpathy,S., Kovar,C., Leal,B., Li,Y., Lichtarge,O.,
Kampal,R., Karpathy,S., Kovar,C., Leal,B., Li,Y., Lichtarge,C.,
Rashid,N.D., Fowland,K., Timms,K.M., Todd,J., Vo,O., Williamson,A.,
Simon,M., Stovall,K., Timms,K.M., Todd,J., Vo,O., Williamson,A.,
Morley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
Direct, Submission
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Homo sapiens XP22 BAC GS-619J3 (Genome Systems Human complete sequence.
Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Apr 18, 1998 this sequence version replaced gi:3056889.
On Apr 18, 1998 this sequence version replaced gi:3056889.
On Apr 18, 1998 this sequence version replaced gi:3056889.
On Apr 18, 1998 this sequence and 2 reads with no ambiguities coverage with a minimum of 2 clones and 3 reads with no or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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                                                                                                                                                         Submitted (18-APR-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-APR-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 144368)
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                                                                                                                                                                                                                                                             Worley, K.C.
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join(52521. .52555,53285. .5
54595. .54744,54795<sub>.</sub> .54875)
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Primates; Catarrhini; Hominidae; Homo.
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complement(8269. 8773)
/rpt_family="Lime1"
8878. .9769
/rpt_family="tlMA2"
complement(21455. 22132)
/rpt_family="tlME3A"
complement(22671. 22766)
/rpt_family="TIGGER2"
22771. 23204
                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1ME3"
complement(10741. .10770)
/rpt_family="(CA)n"
complement(12086. .12112)
/rpt_family="AT_rich"
13204
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complement(2262. .2536)
/rpt_family="LTR16C"
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/rpt_family="AT_rich"
complement(843...1139)
/rpt_family="AluSg"
                                                                                                    /rpt_family="MLT1E"
complement(19499. .19645)
/rpt_family="L2"
                                                                                                                                                                 complement(17077. .17123)
/rpt_family="(CA)n"
complement(18203. .18230)
/rpt_family="MIR"
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complement(14324. .14807)
/note="Region: Similar to gb:x69391 60S ribosomal protein
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/rpt_family="Alux"
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complement(3366. .3465)
/rpt_family="L2"
2621
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/clone="GS-619J3"
/chromosome="x"
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                                                                                                                                                                                                                                                                          15219. .15790
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t_family="L1MA4"
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                                                                                                                                                                                                                                                            _family-"MER4D"
                                                                                                                                                                                                                                                                                                                                                             _family="MSTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family-"AluSq"
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complement(30919, .3103%)
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                            /rpt_family="MER31-internal"
/3140. .43327
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41371. .41804
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/rpt_family="HERVH"
complement(33723...33983)
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complement(23230. .23597)
/rpt_family="TIGGER2"
23587. .23655
                                                                                                                     complement(46607...52764)
/rpt_family="L1PA2"
complement(52787...52832)
/rpt_family="MIR"
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/rpt_family="AT_rich"
complement(42789. .42867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(34589. .35228)
/rpt_family="HERVH"
complement(35229. .37784)
/rpt_family="HERVH"
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/rpt_family="FLAM_A"
44447. .44480
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complement '7"
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complement(29197. .293)
                                                          complement(54583. .54731)
/rpt_fam1ly="MER5A"
                                                                                      complement(53193. .53543)
/rpt_family="MLT1A1"
                                                                                                                                                                                 complement(46263. .46611)
/rpt_family="L1M4"
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45231. .45407
                                                                                                                                                                                                                                                                                                                      /rpt_family~"CHARLIE1"
43780. .44186
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/rpt_family="MSTB"
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complement/200
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complement(34500)
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complement/3307'
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                                                                                                                                                                                                                  rpt_family-"MIR"
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lement/30617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="MER34"
lement/2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _family="MIR"
}, 31035)
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                            Length 144368;
 Indels
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 Gaps
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SOURCE

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RESULT
CNS01RID
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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                                                                                                 Matches
  59916 CAATAGAAGCCATGC 59930
                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                            1 caatagaagccatgc 15
                                                                                                                                                                                                                                                                                                                                                                                                                                         * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12419 13418: contig of 12418 bp in length

* 12419 13418: gap of 1000 bp

* 13419 21210: contig of 7792 bp in length

* 21211 22210: gap of 1000 bp

* 22211 116154: contig of 93944 bp in length

* 116155 117154: gap of 1000 bp

* 117155 142308: contig of 25154 bp in length

* 142309 143308: gap of 1000 bp

* 143309: contig of 26154 bp in length

* 143309 164162: contig of 20854 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-APR-2000) to the EMBL/GenBank/DDBJ databases IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.col1, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage, etc.
Contig order: 6 5 9 7 8, 1000 N's separate segments Contig 6:
length 12418 bp
Contig 5: length 7792 bp
Contig 9: length 93944 bp
Contig 7: length 25154 bp
Contig 7: length 25154 bp
Contig 8: length 20854 bpx
Contig 8: length 20854 bpx
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence of the pieces
* are represented as runs of N. The order of the pieces
* are represented as runs of N. The order of the pieces
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Direct Submission
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HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSO1RID 164162 bp DNA HYDMOMO Sapiens chromosome 14 clone R-98N22, PROGRESS ***, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 164162)
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                       /clone="R-98N22"
29753 c 28500
                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11"
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                                                                                                                           100.0%;
                                                                                                                                                                                                                                                       28500 g 49421 t
                                                                                                      0;
                                                                                                   Score 15; DB 40;
Pred. No. 1.7e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                            4006 others
                                                                                                                                                        Length 164162;
                                                                                                              0,
                                                                                                                 Gaps
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RESULT

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkly, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Grand-Dierre, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Klein, J., Linders, T., Largocque, K., Lehoczky, J., Levine, R.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,
McMan, P., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
Tavers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Mu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 197540)
Birren,B., Linton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted (15-FEB-2000) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA no Apr 3, 2000 this sequence version replaced 91:7249305.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                           * NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L6507
Center clone name: 600_K,3
Center clone cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 197540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 4.3 in Q20 bases; Quality coverage: 4.4 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seg.wi.mit.edu
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ns clone RP11-600K3, WORKING DRAFT SEQUENCE, 21 unordered
1308: contig of 1308 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Lander, E., Abraham, H., Allen, N.,
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sum-of-contigs
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FEATURES
 misc_feature
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37846 46693; contig of 8848 bp in length
46694 46793; gap of 100 bp
46794 53246; contig of 6453 bp in length
53247 53346; gap of 100 bp
53347 53346; gap of 100 bp
66830 66929; gap of 100 bp
66830 79204; contig of 12275 bp in length
79205 79304; gap of 100 bp
79205 79304; gap of 100 bp
79206 79305; contig of 13435 bp in length
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79307 793616; contig of 23178 bp in length
793517 173516; contig of 1338 bp in length
793517 173516; contig of 1338 bp in length
793517 173516; contig of 18318 bp in length
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113352 132820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173517 173616: gap of
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22644 27530: contig of 4887 bp in length
27531 27630: gap of 100 bp
27631 33314: contig of 5684 bp in length
33315 33414: gap of 100 bp
33415 37745: contig of 4331 bp in length
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                                       clone_end:T7
                                                                                                                  /note="assembly_fragment"
27631. .33314
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                                                                                                                                                                                             clone_end:SP6
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/note="assembly_fragment
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12250. .15980
                                                                                                                                                                                                                                                                                                                                                                                       6100.
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/note-"assembly_fragment"
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/db_xref="taxon:9606"
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8681: gap of 100 bp
12149: contig of 3468 bp in length
12249: gap of 100 bp
15980: contig of 3731 bp in length
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Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Caenorhabditis elegans chromosome II clone Y17G7,

    NOTE: This is a 'working draft' sequence.
    NOTE: This is a 'working draft' sequence.
    This record will be updated with the finished sequence
    As soon as it is available and the accession number will

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                 /clone="Y17G7"
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On Mar 31, 2000 this sequence version replaced gi:7362707.
IMPORTANT: This sequence is unfinished and does not necessarily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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1.7e+02;
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Contig_ID: 01113 Length: 4972bp
Contig_ID: 01115 Length: 2372bp
Contig_ID: 01156 Length: 8035bp
Contig_ID: 01215 Length: 1023bp
Contig_ID: 01215 Length: 1123bp
Contig_ID: 01252 Length: 1142bp
Contig_ID: 01252 Length: 1422bp
**NOTE: This is a 'working draft' sequence. It currently
**norsists of 48 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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103487 113064
113065 113864:
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127228 128027:
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77599 86515; contig of 8917 b
86516 87315; gap of 800 bp
87316 90240; contig of 2925 b
90241 91040; gap of 800 bp
91041 92444; contig of 1404 b
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75253 7676
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                                                     145278 146077:
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54704 56636: contig of 1933 b
56637 57436: gap of 800 bp
57437 58475: contin
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93245 94710: contig of 1466 l
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44510 51617; contig of
51618 52417; gap of 8
52418 53903; contig of
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73379 74452: contig of 1074 bp in length
74453 75252: gap of 800 bp
75253 76798: contig of 1546 bp in length
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39771: contig of
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01058
                    28027: gap of 800 bp
145277: contig of 17250 l
16077: gap of 800 bp
148193: contig of 2116 bp
                                                                                                                                127227: conti
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61359: contig of 2
2159: gap of 80
64623: contig of 2
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113064: cont
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58475: contig of
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41584: contig of 1013
884: gap of 800 by
43709: contig of 1325
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1: gap of 800 bp
_6280: contig of 4239 bp in length
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Homo sapiens beta-2 an
AF202305
AF202305.1 GI:6573152
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15; Conservat
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1286)

Rupert, J. L. and Hochachka, P. W.

Beta-2-adrenergic receptor allele frequencies in two native
                                                            Homo sapiens
                                                                        human
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172111 184416: conti
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184417 185216: gap of 1074 bp

185217 186290: contig of 1074 bp

185217 187090: gap of 800 bp

185217 187090: gap of 1009 bp
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155963 16465
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228528 230267: cont
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194706 196042: cont
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168029 168828: gap of 800 bp
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/clone_11b="RPCI-11.1"
39091 c 38984 g 58694 t
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/db_xref="taxon:9606"
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200428: contig of 3586
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232489: contig of 1422
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tive 0; Mismatches
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12110: contig of 3282
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Delectiuse, A. Bourgouin, C., Kiler, A. and Rapoport, G.
Rucleotide sequence and characterization of a new insertion
element, IS240 from Bacillus thuringlensis israelensis
Plasmid 21, 71-78 (1989)
                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis
Bacteria; Firmicutes: Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus
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B.thuringiensis insertion
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2 (bases 1 to 1286)
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M23740.1 GI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rupert, J.L. and Hu
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                  insertion sequence.
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                                                                                                                                                                                                                                                                                                                                                                              thuringiensis israelensis (strain 4Q2-72) DNA, clone
                                                                                                                                                                                aft entry and computer-readable A.Delecluse, 04-APR-1989.
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                                                      /note="left inverted repeat"
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IIMGTFTLCMLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/note="isolated from Quechua speaking Native American"
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                                                                                                      /organism="Bacillus thuringiensis"
/db_xref="taxon:1428"
                                                                                                                                                           Location/Qualifiers
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/db_xref="taxon:9606"
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    Mismatches

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300 a 143 c 176 g 246 t
53 bp upstream of Ball site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 865)
Delecluse, A., Bourgouin, C., Klier, A. and Rapoport, G.
Nucleotide sequence and characterization of a new insertion
element, IS240 from Bacillus thuringiensis israelensis
plasmid 21, 71-78 (1989)
89265213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insertion sequence; transposon.
2 of 2
B.thuringiensis israelensis (strain 4Q2-72) DNA, clone pRX70.
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B.thuringiensis insertion element IS240-B protein gene, complete
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by A.Delecluse, 04-APR-1989.
Location/Qualifiers
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302 a 141 c 178 g 244 t

About 13.5 kb after segment 1; 53 bp upstream of Ball site.
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ilarity 100.0%; Pred. No. 8.4e+02;
Conservative 0; Mismatches 0;
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PLRVKYYLNNMIEQDHRFIKKRILNMLGLKSMQTAVKMIAGIEAMHMVKKGQLKLRAQ
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850. 864
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PLRYKKYLMMIEGDHRFIKKRIRNMLGLKSMQTAVKMIAGIEAMHMYKKGQLKLRAQ
SAQNONRCIHQLFGLTA"
850.865
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db_xref="taxon:1428"
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8.4e+02;
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ALIGNMENTS

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Query Match
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02-OCT-1997; J00982,
24-MAR-1996; JP-072914.
(DAIN ) DAINIPPON PHARM CO LTD.
FUJ11 K, FUTUTANI Y, KAWBShima H
WPI: 97-489627/45.
P-PSDB; W34320,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Disclosure; Page 27-30; 47pp; Japanese.

This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-2 adrenalin receptor subtype coding Beta-2 adrenalin subtype; cyanopindrol; a sthmatic disease; ss.
                                                                                                                Human beta-2-adrenergic receptor cDNA.

Beta-2-adrenergic receptor; human; asthma; beta-agonist; polymorphism; ds.

Homo sapiens.
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21-DEC-1998 (first entry)
                                                                                                                                                                                                                     V52614 standard; cDNA; 3451 BP.
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                                                                                      Location/Qualifiers
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b
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to Gly amino acid change"
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 15;
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 1999
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pr Diagnosing asthma patients predisposed to adverse beta-agonist preactions upon regular administration - by identifying patients processory and the processor and processor and the processor and proces
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Q70084
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Matches 15
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11-SEP-1998; U03908.
26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
BOUShey H, Chinchilli VM, Drazen O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 98-506372/43.
P-PSDB; W75777.
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thuringtensis insecticidal proteins
(Claim 1; Page 7; 9pp; Japanese.
Q70084 is a transcriptional control sequence isolated from Bacillus
(huringtensis (Bt) var. israelensis. It can be used for the expression
of Bacillus thuringtensis insecticidal proteins. The isolation of this
sequence allows the development of a host vector system in Bacillus
thuringtensis and creation of highly insecticidal strains. The new
strains created in this way are not recombinants, the insecticidal
proteins produced using Bt as a host can be applied in agriculture.
Sequence 874 BP; 334 A; 101 C; 161 G; 278 T;
                                                                                                                                                                                                                                                 (SUMO ) SUMITOMO CHEM CO LTD. WPI; 94-275520/34.
                                                                                                                                                                                                                                                                                                26-JUL-1994.
25-FEB-1992; 037748.
25-FEB-1992; JP-037748.
                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis J06205682-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis transcriptional contro-
transcriptional control sequence; expression;
Bacillus thuringiensis israelensis; develop; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1995 (first entry)
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                                                                                                                                                                                                                              Transcriptional control sequence -
                                                                                                                                                                                                                                                                                                                                                                                                              insecticidal strain;
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Pred. No.
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                                                                                                                                                                                                                                  for the expression of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                      develop; host vector system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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 EP-296870-A.
28-DEC-1988.
24-JUN-1988;
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Ellar DJ, Ward ES;
WPI; 89-001322/01.
P-PSDB; P94035.
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28-DEC-1988.
24-JUN-1988; 305772.
26-JUN-1987; US-067653.
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                                                                                                                                                 misc_feature
                                                                                                                                                                                                         biological control agent
                                                                                                                                                                                                                              Delta-endotoxin;
                                                                                                                                                                                                                                            Delta-endotoxin crystal
                                                                                                                                                                                     Bacillus thurigiensis subsp israelensis
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                                                                                                                                                                                                                                                                                                     standard;
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nilarity 100.0%;
Conservative
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   305772
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879. .884
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/label=Shine-Delgarno sequence
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100.0%;
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                                                           b
Shine-Dalgarno
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Best Local Similarity 100
Matches 14; Conservative
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N81490;
O5-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1988.
19-MAR-1987;
19-MAR-1987;
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Ellar (
WPI; 89
X14561 standard; DNA; 1627
X14561;
31-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insecticidal protein gene. Diptera; /
Bacillus thuringlensis israelensis.
Key
                                                                                                                                                                                                                                                                                     protein IG.
The insecticidal protein is highly effective Sequence 4934 BP; 1797 A; 749 C; 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis subsp. 1 microorganisms and plant cells. Disclosure; fig 7; 26pp; Englis
                                                                                                                                                                                                                                                                                                                                                                            A plasmid contg. the gene is isolated by forming from plasmid DNA of B thuringiensis israelensis
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; P81034, P82589.

New insecticidal protein of Bacil

- propd by forming gene library
gene, and transforming host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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P-PSDB; P93715.
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                                                                                                                                                                                                         14;
                                                                                                                                                                                                                          Similarity
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JP-066844.
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Pred. No.
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PD 08-OCT-1998.

PF 01-APR-1998; U06371.

PF 01-APR-1998; U06371.

PR 29-UUL-1997; US-902615.

PR 29-UUL-1997; US-833457.

PR 24-UUN-1997; US-833457.

PR 24-UUN-1997; US-881227.

PR 24-UUN-1997; US-832457.

PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.

PI Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;

PR 40-1998-1999; US-83293-199.

PR WPI; 98-542293/46

PR P-SDB; W98842.

PT New isolated Helicobacter polynucleotides - used to develop products profer the diagnosis, prevention and treatment of Helicobacter profer the diagnosis, prevention and treatment of Helicobacter profer infections and gastrointestinal diseases

PT New isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. CC infections, and gastroduodenal diseases associated with these confections, including acute, chronic, and atrophic gastritis, and peptic colorer diseases, e.g. gastric and duodenal ulcers. They can also be used for detection and diagnosis.

SQ Sequence 1627 BP; 502 A; 286 C; 354 G; 485 T;
 Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local (
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                                                               prepn. of lyase.
Disclosure; Page 8; 9pp; Japanese.
Disclosure; Page 8; 9pp; Japanese.
The sequence is that of the phenylalanine ammonia lyase from Pisum sativum L. The gene may be used to produce P recombinantly. Plants contg. the PAL gene can contain a of phenyl propanoid isoflavonoid.

See also 031985.
Sequence 1707 BP; 496 A; 345 C; 377 G; 489
                                                                                                                                                               26-APR-1991; 097697.
26-APR-1991; JP-097697.
26-APR-1991; JP-097697.
(TAKS) TAKASAGO PERFUMERY CO LTD.
WPI; 93-003497/01.
New phenylalanine ammonia lyase gene from Pisum sativum L
Plasmid contg. gene, and E. coli transformed with plasmid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori GHPO 1548
GHPO protein: "~"'
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18-NOV-1992.
                                                                                                                                                                                                                                                                                    Pisum sativum.
                                                                                                                                                                                                                                                                                                pea; ss
                                                                                                                                                                                                                                                                                                            Phenylalanine
                                                                                                                                                                                                                                                                                                                           Pisium sativum
                                                                                                                                                                                                                                                                                                                                      07-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Q33019
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                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                              ammonia
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la lyase;
            89.3%;
93.3%;
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93.3%;
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Score 13.4; D
Pred. No. 96;
0; Mismatches
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Pred. No. 95;
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PS Claim 1; Page 1956; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically; sequences which are
CC likely to encode antigens have been identified and these polypeptides can
be used in a vaccine composition against S.aureus infection. The
CC saureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC computer readable medium
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                                                                                                                                                                                                            RESULT
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Best Local
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression;
                                                                                                                                                                                                                                                                                                                                                                                        computer
Sequence
WO9730070-A1
                                        Staphylococcus
Key
                                                                                    vaccine;
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07-JAN-1997; 100117.
05-JAN-1996; US-009861
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                                                                       vaccine; Staphylococcal infection; food poisoning;
toxic shock syndrome; ss.
                                                                                                                                                                  T83720;
                                                                                                                                                                              T83720 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxic shock syndrome;
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                                                                                                                                                 l6-JUL-1998 (first entry)
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                            complement (44. .415)
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                                          Location/Qualifiers
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100.0%;
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                                                                                    gene expression;
scaled skin syndrome;
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Best Local
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Wartin wo;
WPI: 98-076485/07.

WPI: 98-076485/07.

Stealth virus nucleic acid molecule - useful to detecting stealth virus, e.g. in chronic fatigue syndrome diagnosis

Example 5: Fig I; 82pp; Bnglish.

V10141-V10210 represent nucleic acid sequences obtained from a patient with a stealth virus infection, namely chronic fatigue syndrome (CFS). Such nucleic acid sequences can be used to detect the stealth virus in medical, veterinary and agricultural diagnostics and in industrial and pharmaceutical biological quality control, e.g. to diagnose a disease associated with the stealth virus.

Sequence 521 BP; 119 A; 146 C; 117 G; 105 T;
                                                                                                                                                                                                                                                       05-JUN 1995; 463115.

05-JUN 1995; US-463115.

23-MAY 1991; US-704814.

20-SEP-1991; US-763039.

22-MAY 1992; US-887502.

23-NOV-1993; US-157811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.

Sequence 417 BP; 134 A; 66 C; 78 G; 132 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 538; 989pp; English.

The present sequence encodes a Staphylococcus aureus protein of unknown function. The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be use to produce vaccines to enable a host to produce specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1997.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
(SMIK ) SMITHKLINE BEECHAM CORP.
Black MT, Burnham MK, Hodgson JE, Kn
Bratt JM, Reichard RW, Rosenberg M,
                                                                                                                                                                                                       Martin WJ; WPI; 98-07
                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1998 (first entry)
Stealth virus nucleic acid in plasmid #4.
Stealth virus; chronic fatigue syndrome; CFS; disease; detection; medical diagnostic; veterinary diagnostic; agricultural diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                    Stealth
                                                                                                                                                                                                                                                                                                                                                                                                                 quality control; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W2775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 caatagaagccat 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                          MARTIN W J.
                                                                                                                                                                                                                                                                                                                                                                                                   virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus strain WCUH29 in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicholas
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Query Match Best Local Matches

13;

Conservative

0,

Mismatches

0;

Indels

0;

Gaps

0

Similarity

86.7%; 100.0%;

Score 13; pred. No.

DB 1; 1.4e+02;

Length 521

S

caatagaagccat 13

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Best Local S
Matches 13
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05-JUN-1995; 465388.

05-JUN-1995; US-465388.

23-MAY-1991; US-704814.

20-SEP-1991; US-763039.

22-MAY-1992; US-887502.

23-NOV-1993; US-157811.

(MART/) MARTIN W J.
                                                                                                        J09075093-A.
25-MAR-1997.
20-FEB-1996; 031987.
21-FEB-1995; US-991696.
29-DEC-1995; US-580545.
(TOYM ) TOYOBO KK.
(UYTE-) UNIV TEXAS TECH.
WPI: 97-239274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 98-31405/27.

WPI; 98-31405/27.

WPI; 98-31405/27.

Stealth virus contained in MRC-5 cell line, ATCC number VR2343 - is useful as a vaccine against chronic fatigue syndrome Disclosure; Fig 1A; 99pp; English.

V11954-V12024 are plasmids which contain fragments of a stealth virus isolated from a patient, D.W. Such stealth virus fragments can be used as vaccine against chronic fatigue syndrome (CFS). This illness causes unexplained fatigue lasting more than 6 months and greater then 50% reduction in an infected persons normal level of activity. The virus causes a cytopathic effect (CFE) to fibroblast cells observed in culture, characterised by the appearance of rounded, slightly enlarged, refractile cells in the culture.

Sequence 521 BP; 119 A; 146 C; 117 G; 105 T;
                                                                                                                                                                                                                                                                                                                                                                                 Cotton fibrous tissue specific gene Gh2.
Fibrous tissue; cotton fibre; cotton flo
Gossypium hirsutum; 88.
Gossypium hirsutum; 88.
Key
Gossypium hirsutum.
Key
37. 447
P-PSDB; W15762. Cotton fibrous tissue gene - used to Improved cotton fibres, and improved Claim 2; Page 22-23; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5753488-A.
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Stealth virus plasmid 4 DN
Chronic fatigue syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stealth virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T60570 standard;
T60570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 86.7%;
Similarity 100.0%;
13; Conservative (
                                                                                                                                                                                                                                                                                                                            /*tag- a
/product- fibrous tissue specific protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB 1; L4; Pred. No. 1.4e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                               produce transformants with yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gossypium barbadense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 521;
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RESULT 1
V37345/c
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                                                                                                                                                                                    Sclaim 1; Page 47; 130pp; English.

Staim 1; Page 47; 130pp; English.

Staim 1; Page 47; 130pp; English region isolated from 75 pneumoniae. Its encoded protein, or agonists of it, 75 pneumoniae. Its encoded protein, or agonists of it, 75 pneumoniae 15 pneumoniae 16 pneumoniae 17 pneumoniae 17 pneumoniae 17 pneumoniae 18 pneumoniae 18 pneumoniae 18 pneumoniae 18 pneumoniae 18 pneumoniae 18 pneumoniae 19 pneumoniae 18 pn
                                                                                                     Query Match
Best Local
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Best Local
                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760567-T60571 represent cotton fibrous tissue genes of the invention. These sequences are specifically expressed during the growth of cotton fibre. The genes were isolated from the polyA RNA of the ovules of a cotton flower of Gossypium barbadense, and G. hirsutum. These sequences, and vectors containing them are used in the preparation of cotton transformants, with improved cotton fibres and improved yield. Sequence 713 BP; 200 A; 131 C; 161 G; 221 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. for ident
of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM BLACK MT, HODGSON JE, KNOWL Reid RH, Zarfos PN; WPI; 98-286586/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1997; U19226.
01-NOV-1996; US-029930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae coding region; ORF; open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W60945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection; prevention; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V37345 standard;
356
                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
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                                      1 caatagaagccat 13
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CAATAGAAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for identifying anti-bacterial(s)
                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae coding region.
ORF; open reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1. .261)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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344
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100.0%;
                                                                                                   86.7%;
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                                                                              Score 13; DB
Pred. No. 1.5
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae - useful, rial(s) for treatment and prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lonetto MA, Nicholas
                                                                          DB 1; ...
1.5e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; L
1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 713
                                                                                                                         Length 740
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                                                                                   Gaps
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RESULT

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NY5239/c.

NY5239; standard; DNA; 1016 BP.

AC Y75239;

DY 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #328.

NY 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #328.

NY Computer readable medium; vaccine; S.aureus infection; immunodetection;

NY Computer readable medium; vaccine; S.aureus infection; sealed skin syndrome;

NY Extaphylococcus aureus.

PN Ex-786519-A2.

PD 30-JUL-1997; 100117.

PR 07-JAN-1997; 100117.

PR 07-JAN-1997; 100117.

PR 07-JAN-1996, IS-009861.

PA (HUMA-) HUMAN GENOME SCI INC.

PA HUMAN GENOM
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      seq
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length: 1000000
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18.269 Million cell updates/sec
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15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                 PCT-US91-00909-3
US-08-633-743-7
US-08-063-743-7
US-08-095-726-19
US-08-095-726-19
US-08-093-577-12
US-08-096-623A-24
US-08-465-388-10
US-08-465-388-10
US-08-665-388-10
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-633-879C-17
US-08-836-0288-1
US-08-363-240A-1105
US-08-363-240A-1105
US-08-363-240A-1141
US-09-092-025A-1
US-08-680-726A-63
US-08-6811-177A-1
US-08-680-726A-63
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Sequence 1, Appli
Sequence 1141, Ap
Sequence 1141, Ap
Sequence 1, Appli
Sequence 3, Appli
Sequence 67, Appli
Sequence 63, Appli
Sequence 64, Appli
Sequence 4, Appli
Sequence 4, Appli
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28 12.4 82.7 4060 2 US-08-164-2928-7 29 12.4 82.7 4060 2 US-08-164-2928-7 30 12.4 82.7 4060 2 US-08-164-2928-7 31 12.4 82.7 4060 5 US-08-845-623-3 31 12.4 82.7 4060 5 US-08-845-623-7 32 12.4 82.7 4060 5 US-08-845-623-7 34 12.4 82.7 7493 1 US-08-212-133A-7 35 12.4 82.7 7493 1 US-08-212-133A-7 36 12.4 82.7 7493 2 US-08-670-707A-5 37 12.4 82.7 7493 2 US-08-670-707A-5 38 12.4 82.7 7493 6 PCT-US94-13200-5 38 12.4 82.7 15328 4 US-08-888-497-3 40 12.4 82.7 15328 4 US-08-888-497-3 41 12 80.0 450 1 US-08-439-537-18 42 12 80.0 450 1 US-08-900-523-28 43 12 80.0 450 1 US-08-398-627-28 44 12 80.0 450 1 US-08-398-627-28	ဂ	ဂ	ဂ	o		a	o	ი											
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1000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	12	12	12	12	12				12.4	12.4	12.4	12.4	12.4	12.4				12.4	12.4
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	450	450	450	68	40	15328	15328	12047	7493	7493	7493	7493	4060	4060	4060	4060	4060	4060	4000
US-08-164-292B-7 US-08-164-292B-7 US-08-845-623-1 US-08-845-623-5 US-08-845-623-7 US-08-845-623-7 US-08-845-623-7 US-08-670-707A-5 PCT-US94-1300-5 US-08-670-707A-5 PCT-US94-1300-5 US-08-888-497-33 PCT-US94-07926-33 US-08-888-497-33 US-08-888-497-38 US-08-776-900C-40 US-08-990-627-28 US-08-990-627-28	N	_	ш	v	-	σ	4	4	σ	w	N	_	σ	ഗ	v	σ	N	N	
	US-08-596-024-4	US-08-398-627-28	US-08-090-523-28	US-08-776-900C-40	US-08-443-957-18	PCT-US94-07926-33	US-08-888-497-33	US-09-022-461-1	PCT-US94-13200-5	US-08-670-707A-5	US-08-474-503-5	US-08-212-133A-7	US-08-845-623-7	US-08-845-623-5	US-08-845-623-3	US-08-845-623-1	US-08-164-292B-7	US-08-164-292B-5	05-08-104-292B-3
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. @@0@##	4, Appl	App	App	App	App	App	App	Appl:	Appli	App1	Appl	Appl:	App1	App1:	Appl:	App11	App1	App1	TOOK

ALIGNMENTS

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RESULT 1
PCT-US91-00909-3
                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9100909
GENERAL INFORMATION:
APPLICANT: Sledziewski, Andrzej Z.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid
TITLE OF INVENTION: Protein-Coupled Receptors
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US91/
FILING DATE: 194.0208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, Dav1d J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
                                   STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States ZIP: 98104-7092
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Patent No.

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               RESULT 3
US-08-963-743-7
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                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08633879C Patent No. 5928922
Sequence 7, Application US/08963743
                                                                                                                                                     Matches
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nissi, Ritva n.
APPLICANT: No. 5928922elainen, Minna K.
TITLE OF INVENTION: '2 SUBUNIT OF PROLYL-4-HYDROXYLASE'
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING SUCH SUBUNIT AND TITLE OF INVENTION: METHODS FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                    OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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| 12 CAATAGAAGCCATGC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 96...272
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Abrams, Samuel B
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pihlajaniemi, Taina
Helaakoski, Tarja I.
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                     100.0%;
                                                                                                                                                                                     93.38;
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                                                                                                                                                       0;
                                                                                                                                                                     Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8389-0041-999
                                                                                                                                                       Mismatches
                                                                                                                                                                     DB 4; Length 2121; 28;
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                            Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 472-9650
TELEFAX: (970) 472-9655
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                              APPLICANT: Ausic
APPLICANT: Brinkha
APPLICANT: Mukha:
APPLICANT: Proff
APPLICANT: Yarge:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JIN, TO APPLICANT: HORNER, Harry T.
APPLICANT: PALMER, Reid G.
APPLICANT: SHOMMAKER, Randy C.
APPLICANT: Soybean Glucanases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/963,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 737 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                CORRESPONDENCE ADDRESS:
                                                                                                TITLE OF INVENTION: Beta-Carotene TITLE OF INVENTION: Genetically Enumber OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                              448 CAATAGCAGCCATGC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Kristine H. Joh
STREET: 123 No. 5952548th
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: JOHNSON, Kristine H. REGISTRATION NUMBER: 36,835 REFERENCE/DOCKET NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                    CITY:
                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
STATE: IL
COUNTRY: USA
                                                ADDRESSEE: Amoco Corp., P. STREET: 200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                           1 caatagaagccatgc 15
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 93.:
14; Conservative
                              Chicago
                                                                                                                                                                                                                                                                9, Application US/08095726 5530188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                               Proffitt, John H
                                                                                                                                                                                           Brinkhaus, Friedh
Mukharji, Indrani
                                                                                                                                              Yarger, James G
Yen, Huei-Che B
                                                                                                                                                                                                                             Ausich, Rodney L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                               89.3%;
93.3%;
                                                                                                                                                                                                                 Friedhelm
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8th College Avenue,
                                                                   Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-1029
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                                                                                                               ne Biosynthesis
Engineered Host
                                                                   and Licensing Dept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 737;
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0;

60680-0703

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TELEPHONE: 3128567180
TELEFAX: 312856472
INFORMATION FOR ESO ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-096-043-16
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Best Local Similarity
Matches 13; Conserv
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GENERAL INFORMATION:
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PATCHTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: GALLOWBY, NO. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Lycopene Biosynthesis in TITLE OF INVENTION: Genetically Engineered Hosts NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                STREET: 200 E
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60680-0703
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                   E: Amoco Corp., Pa
200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brinkhaus, Friedhelm L
Mukharji, Indrani
Proffitt, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yen, Huel-Che B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodney
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                       Patents and Licensing Dept
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-093-577-12
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-096-043-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-093-577-12
                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12,
                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Phytoene Biosynthesis in TITLE OF INVENTION: Genetically Engineered Hosts NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 19-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 60680-0703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brinkhaus, Friedh
Mukharji, Indrani
Proffitt, John H
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               DNA (genomic)
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100.0%;
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Pred. No.
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70;
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Query Match

Best Local Similarity Matches 13; Conserv

Conservative

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Mismatches

Indels

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Gaps

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86.7%; Score 13; 100.0%; Pred. No.

DB 1; Length 39; 70;

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                                                   Best
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                                                                                                                                                                                                    TELEFAX: (312) 655-1501
(NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 655-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                 Local Similarity
les 13; Conserv
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
2 aatagaagccatg 14
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No.
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Mukharji, Indrani
Proffitt, John H.
                                   Conservative
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Yen, Huei-Che B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 07/562,674
03-AUG-1990
                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                         Edward P.
                                              100.0%;
                                                 86.7%; Score 13; DB 1; 100.0%; Pred. No. 70;
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                                 Mismatches
                                 0:
                                                               Length 39;
                               Indels
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; OTHER INFORMATION:
US-08-463-115-10
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US-08-463-115-10
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                                                                 Matches
                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application particul Data: including application DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 199:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSeq Vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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1 caatagaagccat 13
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218 CAATAGAAGCCAT 230
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                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                           TYPE: nucleion STRANDEDNESS:
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                                                                              Local Similarity
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67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILLIAM JOHN MARTIN
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSeq Version 1.5
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100.0%; Pr
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                                                                              Score 13; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                        213/301
                                                                 Mismatches
                                                                                DB 2;
89;
                                                                                             Length 521;
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RESULT 9 US-08-465-388-10

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Sequence 10, Application US/08465388 Patent No. 5753488

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US-08-580-545B-7/c
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                                                                                                         Sequence 7, Application US/08580545B Patent No. 5932713 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: described below:

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/157,811

FILING DATE: No. 5753488ember 23, 1993

APPLICATION NUMBER: 07/887,502

FILING DATE: May 22, 1992

APPLICATION NUMBER: 07/704,814

FILING DATE: May 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: May 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: May 23, 1991
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENERAL INFORMATION:
APPLICANT: WILLIA
                                      APPLICANT:
APPLICANT:
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APPLICATION NUMBER
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Ly
                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 20, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                 218 CAATAGAAGCCAT 230
                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: June 5, 1995
CLASSIFICATION: 435
ROR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon 6 Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                   1 caatagaagccat 13
CANT: YOShihiko, Maekawa
CANT: Randy, Allen
OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
                                                                                                                                                                                                                                                                                                      13;
                                                      Kolchi, Fujisawa
Susumu, Nishiguchi
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                         Yoshihisa, Kasukabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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ISOLATED STEALTH VIRUSES
AND RELATED VACCINES
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100.0%; Pred. No.
tive 0; Mismato
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89;
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RESULT 11
US-09-126-646-1/c
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Patent No. 6001623
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Best Local S
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APPLICANT: BRUN, KIMBERLY A.
APPLICANT: CREASY, CARETHA L
APPLICANT: DUNNINGTON, DAMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202/783-50
TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO:
                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,646
FILING DATE: 31-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bretschnelder, Barry E.
REGISTRATION NUMBER: 28,055
REGISTRATION NUMBER: 04473/068001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DUNNINGTON, DAMIEN J.
TITLE OF INVENTION: HUMAN PROTEIN KINASE H2LAU20
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: fish & Richardson P.C.
STREET: 601 Thirteenth Street, NW
                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202/783-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 601 Thir CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                  STREET: P.O. Box you CITY: Valley Forge
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49 CAATAGAAGCCAT 37
                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 19482
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                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      STATE: PA
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 86.7%; Score 13; 1 Similarity 100.0%; Pred. No. 13; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                & Prestia
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91;
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Prestia, Paul F

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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                    TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/633,879C
FILING DATE: 10-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: N1ssi, Ritva K.
APPLICANT: NO. 5928922elainen, Minna K.
TITLE OF INVENTION: '2 SUBUNIT OF PROLYL-4-HYDROXYLASE
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING SUCH SUBUNIT AND
TITLE OF INVENTION: METHODS FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA
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                 SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                          TELECOMMUNICATION INFORMATION: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Annunen, Pia P.
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                            NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0041-999
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
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STRANDEDNESS:
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610-407-0700
                                                                                                         : 650-493-4935
650-493-5556
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Helaakoski, Tarja I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kivirikko,
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                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
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100.0%;
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Pred. No.
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; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 96...272
; OTHER INFORMATION:
US-08-633-879C-17
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GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: EKK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                  FEATURE:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                    FEATURE:
NAME/KEY: modified_
LOCATION: 56
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JUI
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CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                   LOCATION:
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                     TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                 LENGTH:
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 /mod_base= OTHER
/label= N
/note= "Where N = G,
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Pred. No.
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; HYPOTHETICAL: NO
US-08-836-402B-1
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Best Local Similarity lov.
13; Conservative
                                                          Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/836,402B
FILING DATE: 02-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 44 40 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1836 AATAGAAGCCATG 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Windows 98
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rudiger Hain, Regina Fischer
TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3538
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /label= N
OTHER INFORMATION: /note= "where N = G, A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Gateway 2000
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10591-5144
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                caatagaagccatg
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                                                                                                                                                                                                                                   33 base pairs
                                                             Conservative
                                                                                                                                                                                        linear
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3538
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100.0%; Pred. No.
tive 0; Mismatc
                                                                           82.78;
92.98;
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                                                          Score 12.4; DB 5;
Pred. No. 1.5e+02;
0; Mismatches 1;
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Query Match
Best Local Similarity
Watches 12; Conserve
Search completed: September 12, Job time: 3946 sec
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US-08-363-240A-1055
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US-08-363-240A-1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Courses APPLICANT: McSwiggen, James APPLICANT: Bisgaler, Charles APPLICANT: Pape, Michael APPLICANT: Pape, Michael APPLICANT: Pape, Michael APPLICANT
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: December
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OPERATING SYSTEM: IBM P.C
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STATE: California
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Suite 4700
                                                                                                                                               Conservative
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85.7%;
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OF VASCULAR DISEASES
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Pred. No. 1.5e+02;
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Title:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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seq length: 1000000
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    September 12, 2000, 22:46:49; Search time 1893.64 Seconds (without alignments)
34.931 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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em_est4: *
em_est5: *
em_est5: *
em_est6: *
em_est7: *
em_est10: *
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em_est111: *
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9b_est48:
9b_est
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

120: 121: 122: 123: 124:

gb_gss16:* gb_gss17:* gb_gss18:* gb_gss19:*

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ga88b04.y1 Moss EST library PPU Physcomitrella patens
PEP_SOURCE_ID:PPU161308 5', mRNA sequence.
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W81900
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AW488772
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A2659892 tu01d03.x
A268632 AV368632
A2077922 CIT-HSP-2
AA104807 mo50f12.r
AV322345 AV3685655
AV302345
AII15451 uh86c01.r
AV085655 AV085655
AW501427 UI-HF-BP0
AA511687 V916a01.r
AA869212 V949a04.r
AV241497 AV241497
AQ378683 RPCI-11-1
AQ3988917 RPCI-23-2
AA717083 VU70f12.r
AV067032 AV067032
AW166441 xn53507.x
B68841 CIT-HSP-202
AW488772 UI-M-BH3-AW488772 UI-M-BH3-AW48873 UI-M-BH3-A
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AQ6777734 HS_2190_B
AW674779 ba59e06 y
AQ595678 HS_5459_B
AW561225 9a77b08 y
AQ113165 CIT-HSP-2
AI314125 uj12e03 x
AZ018937 RPCI-33-2
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AW457447 UI-M-BH3-
AW654359 103772 MA
AQ198499 RPCII1-62
AI468443 tg81d07.x
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AQ199592 RPCI11-48
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AV132414 AV132414
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AZ008470 RPCI-23-2
                   cDNA clone
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Local Similarity les 15; Conserv

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
On Jul 8, 1999 this sequence version replaced gi:5422558.
On Jul 8, 1999 this sequence version replaced gi:5422558.
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashiardes as part of th
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco.
Location/Qualifiers
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Eukaryota; Viridiplantae;
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Fax: 314 286 1810
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illarity 100.
Conservative
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//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; CDNA
using Stratagenes 'UniZAP - cDNA synthesis kit'. cDNA
was constructed using an oligo dT primer/linker that
contains a XhoI site within it. Following ds cDNA
synthesis, EcoRI adapters were ligated to the blunt ends
and sample was digested with XhoI. The result is cDNA
synthesis, EcoRI sticky end on one side and a XhoI sticky
end on the other. This cDNA was ligated directionally in
UniZAP arms. The vector is designed containing the
pBluescript sequence as well as lambda DNA and cDNA is
cloned within this pBluescript sequence. The vector was
cloned within this pBluescript sequence. The vector was
cloned within this pBluescript and amplified. The library
was grown in XLIBIUE MRF' cells and amplified. The library
was excised by mass excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
single stranded plasmids that are then packaged (by helper
phage) and secreted out of the host cell as phagemids.
SOLR cells were transformed with phagemids and the library
was plated out on LB-amp plates to select for
transformants. Approximately 1,000,000 colonies were grown
and recovered by using Quiagen Midi prep kit. 2 micro grams of
each library were used to transform DH10B cells by
electroporation."
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/clone_lib="Moss EST library PPU
/tissue_type="protonemata: 7 day
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/lab_host="DH10B"
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                                      Score 15; DB 74;
Pred. No. 1.2e+02;
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   AQ553837.1
GSS.
                                                                                                AQ553837 312 bp DNA RPCI-11-357N10.TJ RPCI-11 Homo sapiens 357N10, genomic survey sequence. AQ553837
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3035541.
Contact: Chie Owa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 219)
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Fax: 81-298-36-9098
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/clone="2700089N23"
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/strain="C57BL/6J"
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Pred. No. 4.5e+0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@filgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pletteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
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The Institute for Genomic Research
Unpublished (1999)
On Dec 15, 1999 this sequence version replaced gi:4574988.
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ008470 398 bp DNA GSS 25-FEB-2000 RPCI-23-246M9.TJ RPCI-23 Mus musculus genomic clone RPCI-23-246M9, genomic survey sequence.
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                                                                                                                                                          Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.
Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., K
Jong, P. and and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 398)
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/db_xref="GDB:7637025"
/db_xref="taxon:9606"
/clone="RPCI-11-357N10"
/clone_lib-"RPCI-11"
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/note="Vector: pBAC63.6; Site_1:
/note="V
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Pred. No. 4.9e+02;
0; Mismatches 0;
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207 CAATAGAAGCCATG 194
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GSS.
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1 (bases 1 to 409)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other, GSSS: RPCIII-1068.TV
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Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ317207 409 bp DNA GSS (RPCI11-106B3.TJ RPCI-11 Homo sapiens genomic clone 106B3, genomic survey sequence.
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                                                                                                                                           9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                   Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ317207
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-246M9"
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/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ199592 435 bp DNA GSS 20-APR-1
RPCII1-48H5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-
48H5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
Clones are darilability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.com). BAC end search page:
Research denetics (info@resgen.com). BAC end search html
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPCI11-48H5.TK
                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Class: BAC ends.
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/clone="RPCI-11-106B3"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                    /organism="Homo sapiens"
/db_xref="cDB:7518220"
/db_xref="taxon:9606"
/clone="RPCI-11-48H5"
/clone_lib="RPCI-11"
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
85 c 112 g 70 t
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/db_xref="GDB:7540346"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI;
RPCII1 Human Male BAC Library"
84 c 95 g 130 t
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 14
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MEDLINE
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2 aatagaagccatgc 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library avallability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgeh.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 1107 row: N column: 14
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HS_5531_B2_G07_SP6E RPCI-11 Human Male BAC Library Homo
sapiens genomic clone Plate-1107 Col-14 Row-N, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
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GSS.
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 471)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           Conservative
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                                                                                                                                                                      /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"

157 t 7 others
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1107 Co1=14 Row=N"
                                                                                                                                                                                                                                                                                                                                                                                              1. .471
                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC Library"
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                                                      93.3%; Score 14; DB 113;
100.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 0;
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5.2e+02;
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                                                                                                                            AW674779 515 bp mRNA EST ba59e06.yl NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900866 similar to SW:SP49_HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTESTALL TO THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2190 row: B column: 14
Seq primer: M13 Reverse
Class: BAC ends
Class: BAC ends
Class: BAC ends
Location/Qualifiers
1 / 100
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HS_2190_B2_A07_MR CIT Approved Human Genomic Sperm Library D
Homo sapiens genomic clone Plate=2190 Col=14 Row=B, genomic
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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E-Coli DH10B"
a 85 c 96 g 166 t 1 others
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/clone_11b="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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/db_xref="taxon:9606"
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Pred. No. 5.4e+02;
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On Jul 7, 1999 this sequence version replaced gi:5407333.
Other_ESTs: ba59e06.xl
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1 (bases 1 to 515)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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HS_5459_B2_D06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1035 Col=12 Row=H, genomic survey
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Location/Qualifiers
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                                                        On Dec 15, 1999 this sequence version replaced gi:4215181.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
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401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                             scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17),
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/db_xref="taxon:9606"
/clone="IMAGE:2900866"
/clone=11b="NIH_MGC_10"
/cell_line="MGC36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies."
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1035 row: H column: 12
Seg primer: T7
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Location/Qualifiers
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                                                                                                                                                                                                                                                                    Unpublished (1999)
on Jan 6, 2000 this sequence version replaced Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis,
                                          Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk) seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariaceae; Physcomitrella.

1 (bases 1 to 519)
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                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                Email: est@watson.wustl.edu
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/note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"

120 c 102 g 152 t 4 others
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/db_xref="taxon:9606"
/clone="plate=1035 Col=12 Row=H"
/clone_lib="RPCI-11 Human Male BAC Library"
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0; Mismatches
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5.4e+02;
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                                                                                                                                                                                                                                                                                    Louis,
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                                                                                                                                                                                                                                                                                       MO 63108, USA
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FEATURES

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COMMENT
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                                                                                                                                                                                                                 TITLE
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Best Local
                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 CAATAGAAGCCATG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ113165 539 bp DNA GSS 29-AUG-199 CIT-HSP-237509.TF CIT-HSP Homo sapiens genomic clone 237509, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ113165.1
GSS.
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 539)
Adams, M.D.; Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                               Unpublished (1998)
Other_GSSs: CIT-HSP-237509.TR
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                               Use of a random human BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ113165
                                                                                                                                                                                                                                          Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Construction of the cDNA library was carried out using Stratagenes 'UniZAP - CDNA synthesis kit'. cDNA was constructed using an oligo dT primer/linker that contains a XhoI site within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is cDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence. The vector was cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XLDBlue MRF' cells and amplified. The library was grown in XLDBlue MRF' cells and applified. The library was excised by mass excision using Stratagens 'Mass excision kit' that uses exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."
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/clone="pep_SOURCE_ID:ppU140116"
/clone_lib="Moss EST library ppU"
/tissue_type="protonemata: 7 day old tissue
ammonium-grown"

    519
    organism="Physcomitrella patens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:3489286
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                                                                                                                                                                                                            End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                Zhao,S., Bass,S., Linher,K., Golden,K.,
E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 74; 1
5.4e+02;
                        MD 20850, USA
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BASE COUNT
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AUTHORS
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VERSION
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AI314125/c
                                                                                                                                                                                          FEATURES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI314125 560 bp mRNA EST 17-DEC-199 uj12e03 x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE: 1907836 3', mRNA sequence.
                                                                                                                                                                                                       Seq primer: custom primer used High quality sequence stop: 501
                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
TMAGE Consortium (info@image.linl.gov) for further i
                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                      Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI314125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301 838 0208
Email: mdadams@ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI314125.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .539
                                                                          /db_xref="taxon:10000"
/clone="IMAGE:1907836"
/clone_lib="Sugano mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="237509"
/clone_lib="CIT-HSP"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                                                                                                                                 /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                              /sex="female"
                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to 560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No.
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o. 5.5e+02;
0;
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                                                                              kidney mkia"
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RESULT 14
AZ018937/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZU18937 561 bp DNA GSS 25-FEB-2000 RPCI-23-298P23. TV RPCI-23 Mus musculus genomic clone RPCI-23-298P23, genomic survev seguence
                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 298 row: P column: 23
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Dec 15, 1999 this sequence version replaced gi:4575467. Other_GSSs: RPCI-23-298P23.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sakinret, B., Levins, M., Mcgann, S., Tsegaye, G., Jong, P. and and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ018937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 838 0200
301 838 0208
1: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilgated to a Draill adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DrailI sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                          Location/Qualifiers
1. .561
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ScoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                                                                        /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                           /db_xref="taxon:10090"
/clone="RPCI-23-298P23"
                                                                                                                                                                            /strain="C57BL/6J"
                                                'lab_host="DH10B"
                                                                                                                                                                                                 organism="Mus musculus"
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Pred. No.
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. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MD 20850, USA
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REFERENCE AUTHORS

VERSION ACCESSION DEFINITION

KEYWORDS

COMMENT

TITLE JOURNAL

FEATURES

Query Match

Score 14;

DB 42;

Length 618;

밁

Matches

BASE COUNT ORIGIN

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REFERENCE
AUTHORS
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SOURCE
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LUO1063.x1 NCI_CGAP_PT28 Homo sapiens cDNA clone IMAGE:2249765 3'
tsimilar to gb:M94556 SINGLE-STRANDED DNA-BINDING PROTEIN
MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
seq primer: -40UP from Gibco
High quality sequence stop: 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/Linu at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index Unpublished (1997) Unpublished (1997) Unpublished (1997) On Oct 8, 1998 this sequence version replaced gi:3728902. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI659892.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      162
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                 'note-"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
mormalized library NCI_CGAP_P122 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was pCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 147 c 104 g 203 t 2 others
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2249765"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 to 618)
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                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                    'dev_stage="adult"
                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                      clone_lib="NCI_CGAP_Pr28"
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100.0%; Pred. No.
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. 5.5e+02;
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Best Local Smilarity 100.04; Fred. No. 5.6e-02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 castspangocaty 14

pb 562 CANTHOLAGOCATE 549

Search completed: September 12, 2000, 22:46:55

Job time: 3787 sec
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Title:
Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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gb_ph:*
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643: 654: 655: 667: 677: 688: 700: 711: 723: 733:	
22222221116764	 gb_htg7:* em_htg1:* em_htg2:* em_htg3:* em_hum5:* gb_pt3:* gb_htg8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

24	23	22	21	20	c 19	18	17	16	15	14	13	12	11	10	9	8	7	6	տ	4	w	2	c 1	Result No.
13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	Score
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4343	4197	4190	3780	3458	2426	2339	2165	1970	1959	1340	1290	1290	1242	939	915	911	911	911	910	906	904	904	487	Query Match Length
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MMTCAN	RATMTA	RSB2AR	RNU35448	HUMADRBRA	AF047430	IRO29222	AAU86080	HSBARR	RATADBC	CEPHOCAR	AF203386	AF169225	AF022953	AF027231	AF027230	AF027228	AF027227	AF027226	AF027233	AF027225	AF027251	AF027232	AF179732	ID
X92864 M.musculus	L39264 Rattus norv	X17607 Rat beta-2	U35448 Rattus norv	J02960 Human beta-	AF047430 Sinorhizo	AL109671 Homo sapi	U86080 Aedes aegyp	X04827 Human mRNA	J03024 Rat beta-ad	x76113 C.elegans m	AF203386 Homo sapi	AF169225 Homo sapi	AF022953 Homo sap1	AF027231 Cepphus g	 AF027230 Cepphus g 	AF027228 Cepphus g	AF027227 Cepphus g	AF027226 Cepphus g	AF027233 Cepphus g	AF027225 Cepphus g		AF027232 Cepphus g	AF179732 Pan trogl	Description

Query Match Best Local S Matches 13

l Similarity 13; Conserv

100.0%; ilarity 100.0%; Conservative

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BASE CO

COUNT

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2 (bases 1 to 487)
Giorgi,D.G. and Rouquier,S.P.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, U
1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
                                                                                                                                             /product="01factory receptor"
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                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                               cocation/Qualifiers
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AC021969
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                               Score 13; DB 9;
Pred. No. 6.1e+02;
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                 Mismatches
                                                                                                                    163
                   0;
                                                   Length 487;
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A68743 Sequence 1
X99450 H.sapiens p
AF037062 Homo sapi
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Aves; Neognathae; Charadrilformes; Alcidae; Cepphus
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Sequence variation in the guillemot (Alcidae: Cepphus mitochondrial control region and its nuclear homolog Mol. Biol. Evol. 15 (1), 61-70 (1998) 98152305
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Mitochondrion Cepphus grylle grylle
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
          2 (bases 1 to 904)
Kidd,M.G. and Friesen,V.L.
Direct Submission
Submitted (29-SEP-1997) Biology, Queen's University, Kingston,
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/organelle="mitochondrion"
/isolate="CGA-SD-0001"
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/db_xref="taxon:78224"
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/gene="PTR207"

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Pan troglodytes chimpanzee AF179732.1

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Pan troglodytes olfactory AF179732

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Kidd,M.G. and Friesen,V.L.

Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
Mol. Biol. Evol. 15 (1), 61-70 (1998)
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AF027225 AF027225.1 GI:3264873
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Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
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Kidd,M.G. and Friesen,V.L.
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/sub_species="ultimus"
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/organelle="mitochondrion"
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AF027226 AF027226.1 GI:3264874
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Submitted (29-SEP-1997) Biology,
K7L 3N6, Canada
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Kidd, M.G. and Friesen, V.L.
Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
Mol. Biol. Evol. 15 (1), 61-70 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
                                                                                                             Direct Submission Submitted (29-SEP-1997) Biology,
                                                                                                                                                                                                                                                                            Mitochondrion Cepphus grylle ultimus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadrilformes; Alcidae; Cepphus.
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                                                                                                                                             2 (bases 1 to 911)
Kidd, M.G. and Friesen, V.L.
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/organism="Cepphus grylle ultimus"
/organelle="mitochondrion"
/isolate="CGU-DS-2190"
/sub_species="ultimus"
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236 c 141 g 271 t 30 others
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/organelle="mitochondrion"
/isolate="CGA-SD-0002"
                                                                                ocation/Qualifiers
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/db_xref="taxon:78224"
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AF027227
AF027227.1 GI:3264875
AFU27228 911 bp DNA VRT 08-JUL-1998 Cepphus grylle islandicus isolate CGI-FI-002B mitochondrial control region, partial sequence.
AF027228
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Kidd, M.G. and Friesen, V.L.
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Eukaryota; Metazoa; Chordata; Craniata; Veri
Aves; Neognathae; Charadriiformes; Alcidae;
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/note="common name: black guillemot"
<1. .>911
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823. .857
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239 c 138 g 270 t 26
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/organelle="mitochondrion"
/isolate="CGI-FI-002A"
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237 c 137 g 266 t 41
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                                                                                                                                                                                                                                                                                                                                                          /sub_species="islandicus"
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dae; Cepphus
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Mitochondrion Cepphus grylle islandicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
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Submitted (29-SEP-1997) Biology,
K7L 3N6, Canada
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neggnathae; Charadriiformes; Alcidae; Cepphus.
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Cepphus grylle mandtli isolate CGM-SV-0001 mitochondrial control
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Kidd, M.G. and Friesen, V.L.
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                                                                                                                              Direct Submission Submitted (29-SEP-1997) Biology, K7L 3N6, Canada
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Kidd, M.G. and Friesen, V.L.
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823. .857
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/isolate="CGI-FI-002B"
/sub_species="islandicus"
/db_xref="taxon:78226"
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228 c 138 g 268 t 50
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               /sub_species="mandtii"
/db_xref="taxon:78227"
                                                 /organelle="mitochondrion"
/isolate="CGM-SV-0001"
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                                                                                   /organism="Cepphus grylle
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/note="common name: black guillemot"
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AF022953.1 G:
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Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
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Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
Mol. Biol. Evol. 15 (1), 61-70 (1998)
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Kidd, M.G. and Friesen, V.L.
Direct Submission
Submitted (29-SEP-1997) Biology,
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/note="mitochondrial control region"
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250 c 144 g 276 t 9 o
                                                                                                                                                                                                                                                                                                                                                         /organism="Cepphus grylle mandtii"
/organelle="mitochondrion"
/18olate="CGM-SV-0002"
/sub_species="mandtii"
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AF169225.1 GI:5714687
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Liggett, S.B. and Green, S.A.
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/product="beta2-adrenergic receptor"
/protein_id="AAB82148.1"
/db_xref="GI:2570527"
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/db_xref="taxon:9606"
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Rupert, J.R. and Hochachka, P.W.
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Rupert,J.R. and Hochachka,P.W.
Beta-2-adrenergic receptor allele frequencies in two native
                                                                Unpublished (bases 1 to 1290)
2 (bases 1 to 1290)
Rupert,J.L. and Hochachka,P.W.
Direct Submission
Submitted (09-NOV-1999) Zoology, University of British Columbia,
Submitted (09-NOV-1999) Zoology, University of British Columbia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     American
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1290)
Rupert,J.L. and Hochachka,P.W.
                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                          Beta-2 adrenergic receptor allele frequencies in two Native
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        AF203386.1
                                                                                                                                                                                                      American populations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
milarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="beta-2-adrenergic receptor"
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/product="beta-2-adrenergic receptor"
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AFQELLCLRRSSLKAYCNGYSSNGNTGEQSGYHVEQEKENKLLCEDLFGTEDFVGHQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="5q31-q33"

/cell_type="lymphocyte"

/tissue_type="blood"

/note="isolated from a Quechua speaking native American

heterozygous for a known C/T mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVPSDNIDSQGRNCSTNDSLL"
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /replace="C/T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/db_xref="taxon:9606"
                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               p DNA PRI 28-DEC-1999 adrenergic receptor (ADRB2) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13; DB 39;
Pred. No. 6.3e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of British Columbia, BC V6T 1Z4, Canada
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AUTHORS
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SOURCE .
ORGANISM
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CEPHOCAR
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VERSION
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Best Local
                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                            MEDLINE
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                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphate carrier.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                      1 (bases i to 1340)
Walker, J.E.
Direct Submission
Submitted (10-NOV-1993) J.E. Walker, MRC Lab of Molecular Biology,
Hills Road, Cambridge CB2 2QH, UK
2 (bases 1 to 1340)
Runswick, M.J., Philippides, A., Lauria, G. and Walker, J.E.
Extension of the mitochondrial transport superfamily: sequences of
five members from the nematode worm Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.elegans mRNA for X76113
                                                                                                                                                                                                                                                                                 Runswick, M.J., Philippides, A., Extension of the mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X76113.1 GI:472905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEPHOCAR
                                                                                                                                                                                                                                            DNA Seq. 4 (5), 281-291 (1994)
                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                               five members
                                                                                                                                                                                                                                                                                                                        (bases 1 to 1340)
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345 c 333 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="beta-2 adrenergic receptor"
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVLMVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSRVFQEAKROLOKIDKSEGRFHVONLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="5q32-q34"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ADRB2"
26. .1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="5"
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5. .1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="ADRB2"
                                                                                                                                                 /organism="Caenorhabditis
/db_xref="taxon:6239"
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                             /germline
                                                                                                                                                                                        1. .1340
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                                                                                                                                                                                                                                                                 from the nematode worm, Caenorhabditis elegans
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phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carrier protein.
                                                                                                                                                                                                                                                                                   Lauria, G. and Walker, J.E. transporter super-family: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quechuan-speaking Native American"
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                                                                                                                                                                       elegans"
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polyA_site
BASE COUNT :
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AUTHORS
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ORIGIN
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VERSION
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RATADBC
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MEDLINE
Query Match 100.0%; Score 13; DB 12; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                            1 bp
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Rat beta-adrenergic receptor mRNA, complete cds.
J03024
J03024.1 GI:202710
beta-adrenergic receptor.
Beta heart, CDNA to mRNA, (library of Clontech), clone
lambda RHB-DAR.
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Gocayno,J., Robinson,D.A., FitzGerald,M.G., Chung,F.-2., Kerlavage,A.R., Lentes,K.-U., Lai,J., Wang,C.-D., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primary structure of rat cardiac beta-adrenergic and muscarinic chollnergic receptors obtained by automated DNA sequence analysis: Furthur evidence for a multigene family Proc. Natl. Acad. Sci. U.S.A. 84, 8296-8300 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aft entry and computer-readable sequence for [1] kindly provided
A.Kerlavage, 20-OCT-1987.
                                                                                                                          466 a 4
p upstream
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86. .1024
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1312. .1340
a 359 c 268 g 366 t
                                                                                                                                                                                                                                                    /protein_id="AAA40675.1"
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                                                                                                                                                                          VNCOGTVPSLSIDSQGRNCNTNDSPL"
                                                                                                                                                                                                    IIMGTFTLCWLPFFIVNIVHVIRANLIPKEVYILLNWLGYVNSAFNPLIYCRSPDFRI
AFQELLCLRRSSSKTYGNGYSSNSNGRTDYTGEQSAYQLGQEKENELLCEEAPGMEGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"ADB mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="beta-adrenergic receptor"
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m of HindIII site.
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Search completed: September 12, 2000, 23:03:24 Job time: 3996 sec

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Minimum DB
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Sequence 69 BP; 19 A; 10 C; 18 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-S.aureus vaccines
Claim 1; Page 2172; 3271
This sequence represents
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EP-786519-A2.
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                            The present sequence represents a nucleic acid sequence identified in the course of the invention, and expressed in lung, brain, kidney, heart muscle, liver, placenta, small intestine and activated T-cells. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1998.
27-FEB-1997; U03159.
27-FEB-1997; WO-U03159.
                                                                                                                                                                                                                                                               Novel human immunomodulatory poly:peptide(s) yeast RAD50 or Drosophila Septin-2 proteins Disclosure; Page 119; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Dolganov G;
WPI; 98-481207/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human homologue; yeast RAD50; Drosophila Se
immunomodulatory activity; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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RESULT RE
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Q65486
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Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2012; 2084pp; English.

A computer readable medium has been developed which has recorded on it a computer readable medium has been developed which has recorded on it a computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for disposing Enterococcual infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis in the progression of the product of the computer of the product of the progression of the product of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides and polypu-
used to develop products for the detection of Enterococcus
use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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04-MAY-1998; U08985
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can be used in vaccines to prevent or attenuate an Enterococcal
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signal_peptide
                                                                Homo sapiens.
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12; Conserv
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ilarity 100.0%;
Conservative
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ng Elk-L
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   Location/Qualifiers
1. .72
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100.0%; Pr
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ein; elk; li
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ligands;
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                                                                                                                                        receptor ligand. cell growth; differentiation;
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1.1e+
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1.2e+02;
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13 Baum PR, Beckmann MP, Lyman S;

14 MPI; 94-183415/22.

15 MPI; 94-183415/22.

16 P-PSDB; R55059.

17 New DNA encoding ligand for elk tyrosine kinase receptor - also

17 related polypeptides, vectors, antibodies and probes, useful e.g.

18 P-PSDB; R55059.

19 related polypeptides, vectors, antibodies and probes, useful e.g.

10 related polypeptides, vectors, antibodies and probes, useful e.g.

10 related polypeptides, vectors, antibodies and probes, useful e.g.

10 related polypeptides, vectors, antibodies and probes, useful e.g.

20 related polypeptides, vectors, antibodies and probes, useful e.g.

21 related polypeptides, vectors, antibodies and probes, useful e.g.

22 related polypeptides, vectors, antibodies and probes, useful e.g.

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26 related polypeptides, vectors, antibodies and probes, useful e.g.

27 related polypeptides, vectors, antibodies and probes, useful e.g.

26 related polypeptides, vectors, antibodies and probes, useful e.g.

27 related polypeptides, vectors, antibodies and probes, useful e.g.

28 related probes, vectors, antibodies and probes, useful e.g.

29 related probes, vectors, antibodies and probes, useful e.g.

20 related probes, vectors, antibodies and probes, useful e.g.

20 related probes, vectors, antibodies and probes, useful e.g.

21 related polypeptides, vectors, antibodies and probes, useful e.g.

21 related probes, vectors, antibodies and probes, useful e.g.

22 related polypeptides, vectors, antibodies and probes, useful e.g.

22 related polypeptides, vectors, antibodies and probes, useful e.g.

23 related polypeptides, vectors, antibodies and probes, useful e.g.

24 related polypeptides, vectors, antibodies and probes, useful e.g.

25 related polypeptides, vectors, antibodie
                DNA coding for neurotrophic human elk ligand cytokine - useful as probe to isolate other elk ligand sequences (Claim 7; Columns 27-30; 18pp; English.

The present sequence encodes the human cytokine elk-ligand (elk-L), which binds a member of the tyrosine kinase receptor family. Elk-L cachibits neurotrophic and neuroprotective properties, and has a calculated mol. wt. 35180 daltons and a pl of 9.006. The elk-L cDNA, isolated from a human placental cDNA library, can be radiolabelled and used as a probe for isolating other mammalian clk-L cDNA. Elk-L can be used to treat neural tissue disorders, and as a neural culture reagent, while immunogenic fragments of elk-L can be used to generate specific anti-elk-L antibodies.
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Best 1
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30-APR-1996.
13-NOV-1992; 977693.
13-NOV-1992; US-977693.
15-MAR-1994; US-213403.
[IMMV] IMMUNEX CORP.
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15-NOV-1993;
13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal_peptide
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Human cytokine elk-ligand (elk-L) cDNA.
Human; cytokine; elk-ligand; elk-L; tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T28770 standard;
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US-977693.
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73. .1038
/*tag= c
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73. .1038
/*tag=_ b
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1. .72
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Pred. No.
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antibodies.
C; 309 G
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Claim 7; Columns 27-30; 18pp; English.

The present sequence encodes a human elk ligand (elk-L) protein,
which binds elk, has a calculated molecular weight of 35180 and an
isoelectric point of 9.006. Elk-L is a cytokine that can be used to
test cells for elk expression, measure the biological activity of
elk, purify elk by affinity chromatography and as a neuroprotective
agent to treat diabetic, hereditary and nutritional neuropathies
and neurodegenerative diseases. It may also be added to tissue
cultures to prolong the life of neurons. The elk-L cDNA was
isolated from a human placental cDNA library, and is present as a
CDNA insert in the recombinant vector deposited in strain
                                                                                                                                                            Query Match
Best Local S
Matches 12
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1992;
13-NOV-1992;
15-MAR-1994;
01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human elk ligand cDNA. Human; elk; ligand; elk-L; cytokine; testing; measur purification; neuroprotection; treatment; diabetic; nutritional; neuropathy; neurodegenerative disease; tissue culture; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV) IMMUNEX CORP.
Baum PR, Beckmann MI
WPI; 97-271366/24.
  Human elk-L coding sequence.
Human; elk-L; cytokine; liga
extracellular domain; immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5627267-A.
06-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                             Human elk ligand protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal_peptide
                                    06-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T69766
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12; Conserv
                                                          standard;
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                                                                                                                                                            l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        W19249
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                                                                                                                                                           92.3
illarity 100.
Conservative
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US-977693.
US-213403.
US-458077.
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73. .1038
/*tag= c
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1. .72
                                                                                                                                                                                                                    BP;
                                                          CDNA
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e; ligand; tyrosine kinase receptor; fusion protein; immunoglobulin; neurological disease; ss.
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                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                             Lyman
                                                                                                                                                                         .08
                                                            mRNA;
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                                                                                                                                                                                                                   Α;
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Pred. No.
                                                                                                                                                            Score 12; DB Pred. No. 1.3
0; Mismatches
                                                           1041
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                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testing; measuring;
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                                                                                                                                                         DB 1; Lc.,
J. 1.3e+02;
O;
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1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                             therapeutic
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                                                                                                                                                                                Length 1041
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RESULT V1226 V1 DE 226 V1 DE 226 V1 DE 226 V1 DE Ht KW Ht KW Ht KW HT KW HT KW HT KW TH KW
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Best Local S
Matches 12
                                                                                                         15-MAR-1994; US-213403.
13-NOV-1992; US-977693.
02-JUN-1995; US-460741.
12-NOV-1996; US-747240.
(IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1997.
02-JUN-1995;
15-MAR-1994;
13-NOV-1992;
02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble fusion proteins of human elk-ligand and Fc immunoglobulin fragment - and their dimers and oligomers, useful as neuro-protectants and neurotrophic agents Example 3; Columns 27-30; 18pp; English.

This is the nucleotide sequence encoding the human elk-L protein, a new cytokine that is the ligand for the elk tyrosine kinase receptor. The extracellular domain of the protein (amino acids 1-213) is used to generate a fusion protein comprising the Fc polypeptide of the human immunoglobulin G1 (extending from the hinge region to the C-terminus). The fusion protein (which has the same activities as the natural elk-L protein) has neuroprotective and neurotrophic activity so is potentially useful for treating a wide range of neurological diseases.

Sequence 1041 BP; 239 A; 306 C; 309 G; 187 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
CDS
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V15226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5670625-A.
                       Baum PR, Beckmann MP, Lyman WPI; 98-206621/18. p-PSDB; W44323. Antibodies to elk ligand pol
                                                                                                                                                                                                                                                   US5728813-A.
17-MAR-1998.
                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human elk-L encoding cDNA.
Human; elk-L; elk ligand; cytokine; antibo
tyrosine kinase receptor; neural disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
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    receptors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                           12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beckmann MP,
    useful
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; US-213403.
; US-977693.
; US-460741.
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73. .1038
/*tag= c
                                                                                                                                                                                                                                                                                                                /*tag= a
1. 72
/*tag= b
73. 1038
/*tag= c
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1. .72
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                                                                                                                                                                                                                                                                                           /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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  ligand polypeptides for treating neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                  "elk-L"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; cell surface receptor;
       disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3e+02;
0;
                            bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trophic mechanism; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1041;
                            tyrosine kinase
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RESULT
V08374
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellulose synthase PosA3 concellulose synthase; cotton; Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V08374 stand
V08374;
08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Column 27-29; 17pp; English.
The present sequence encodes human elk-L (elk ligand). The present invention describes antibodies to elk-L polypeptides. The elk-L protein is known to be neuroprotective exhibiting its effect through a trophic mechanism. Examples of diseases that may be treated with elk-L include neuropathies e.g. diabetic, hereditary and nutritional neuropathies, neurodegenerative diseases and other diseases characterised by loss of function or degeneration of neurons.

Sequence 1041 BP; 239 A; 306 C; 309 G; 187 T;
                                                                               X13928 stand
X13928;
31-MAR-1999
                                                                                                                                                                                                                                                                                                                        This sequence encodes a cellulose synthase of the invention. The DNA car be used for controlling cellulose synthesis in a cell by introducing the DNA into the cell, expressing RNA with a nucleotide sequence homologous to the DNA or a nucleotide sequence complementary to the DNA. The cells are prokaryotic cells i.e. acetobacterium and/or eukaryotic cells such a years i.e. Saccharomyces spp., plant cells (cotton plants) and cultured years i.e. Saccharomyces spp., plant cells (cotton plants)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISN ) NISSHINBO IND I AOTSUKA S, Hasegawa O, WPI; 98-559440/48. P-PSDB; W73310.
                     GHPO protein; Helicobacter peptic ulcer disease; ss. Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding cotton cellulose synthase proteins - useful controlling cellulose synthesis in prokaryotic or eukaryotic Example 5; Page 36-37; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-875575-A2.
04-NOV-1998.
31-MAR-1998; 302489.
01-APR-1997; JP-083133.
                                                    H. pylori GHPO GHPO protein; P
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                 cells of
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| | | | | | | | | | | |
| CCAATGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                         standard; DNA; 1516
                                                                                                                                                                                                                                                                                                                 mammals etc.
                                                                                                                                                                                                                                                                                                   1086 BP;
                                                                                                                                                                                                                   J2.38; Score 12;
ilarity 100.08; Pred. No.
Conservative 0; Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                 (first entry) PO 701 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA to mRNA; 1086
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                                                                                                                                                                             32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi T, Ihara
                                                                                                                                                                                                                                                                                                 290 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stop codon given"
                                                                                                           ВP
                                                       infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12;
Pred. No.
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J. 1.3e+02;
O;
                                                     gastroduodenal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲;
                                                                                                                                                                                                                                                 1 B
                                                                                                                                                                                                                                                .3e+02;
                                                                                                                                                                                                                                                                                                      296
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                                                                                                                                                                                                                                                           Length 1086
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                                                                                                                                                                                                                                                                                                                              karyotic cells such as plants) and cultured
                                                                                                                                                                                                                                                                                                      294
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                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                           cells
                                                        gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT J
Q20231C J
Q2023C J
Q2020C J
Q2
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increasing starch content of plants, esp. potato and tomato - by introducing into genome a gene for ADP-glucose pyro-phosphorylase activity, fused to plastid transit gene
Bisclosure; Fig 5; 120pp; English.
The inventors claim a method for inc. the starch content of a plant by inc. its ADP glucose pyrophosphorylase (ADPGPP) activity. The method uses a recombinant DNA molecule encoding a fusion protein of amino-terminal plastid transit peptide and ADPGPP. The ADPGPP gene is the glg gene of E. coli Kl2, or its mutant form gig Cl6 (which causes accumulation of more glycogen and has higher affinity for ADP glucose in the absence of an activator). A pref. plastid transit peptide, designated CPP1, is derived from the sskubisco la gene of from the nopaline synthase (NOS) gene.
Sequence 1575 BP; 462 A; 322 C; 365 G; 426 T;
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Best L
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08-OCT-1998.
01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9119806-A.
26-DEC-1991.
07-JUN-1991: U04036.
18-JUN-1990: US-539763.
07-JUN-1991: US-709663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter Infections and gastrointestinal diseases Claim 1; Page 114-116; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H. pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic closer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used detection in an disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q20231 ;
Q20231;
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(HUMA-) HUMAN GENOME SCI INC.

Al-Garawi A, Kleanthous H, Miller C, Oomen RP WPI; 98-542293/46.

P-PSDB: W98209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potato.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection and diagnosis. Sequence 1516 BP; 4
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3. .1568
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 C;
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,. 1.4e+02;
0;
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RESULT 13
Q80085/c
ID Q80085;
CROORS;
DT Q80085;
DE ADDGCP small subunit gene.
KW ADP-glucose-pyrophosphorylase;
KW potato; Escherichia coll; swee
KW storage; ds:
Solanum tuberosum.
FH Key Location/Quall
FT cds /*tag- a
PN W09428149-A.
PF CB 3. 1568
FT W09428149-A.
PF 18-MAY-1994; U05275.
PR 28-MAY-1994; U05275.
PR (MONS) MONSAWTO CO.
PI Barry GF, Kishore GM, Stark
DR WP; 95-022820/03.
PR P-SDB; R66239,
PT Transforming potato plants to
PT pyro-phosphorylase - improvit
PT and extending dormancy of story
PT pyro-phosphorylase - improvit
PT and extending dormancy of story
PSDB; R66239,
CC Apotato tuber ADP-glucose-pyr
CC sequences from the 1st exon od
CC full-length cDNA of the same c
CC Q80087-89 were used to: introc
CC codon to facilitate cloning in
CC vectors; to introduce a Saci 3
CC and to remove an internal Bg11
CC expressed in E. coli from the
CC cassette. An initiating ATG c
CC given in Q80090 to express the
SQ Sequence 1575 BP; 460 A;
                                                                                                                                                                                                                  RESULT 14
Q85025/c
ID Q85025
FFH OKW DAC
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Disclosure; Page 48-50; 72pp; English.

Subunit gene (given in Q80085) was assembled by addition of sequences from the 1st exon of the genomic clone with a nearly full-length cDNA of the same gene. The primers given in Q80087-89 were used to: introduce a BgIII+NCOI site at the ATG codon to facilitate cloning into E. coll and plant expression codon to facilitate cloning into E. coll and plant expression codon to facilitate cloning into E. coll and plant expression codon to remove an internal BgIII site. The assembled gene was expressed in E. coll from the recA promoter in a PrecA-gene10L cassette. An initiating ATG codon was placed using the primer given in Q80090 to express the mature gene.

Sequence 1575 BP; 460 A; 324 C; 365 G; 426 T;
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                enzyme engineering; c feedstuff; food; ds. Solanum tuberosum. Key Locat cds 3..1
                                                                                           ADP-glucose-pyrophosphorylase small subunit gene.
Potato tuber: ADP-glucose-pyrophosphorylase small subuni
site-directed mutagenesis; Escherichia coli; transgenic
enzyme engineering; cloning; crop improvement; oilseed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADPGPP small subunit gene.

ADP-glucose-pyrophosphorylase; ADPGPP; glgC; transgenic plant; potato; Escherichia coli; sweetness; dormancy; crop improvement;
                                                                                                                                                                             23-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                        19 CCAATGGAAGCC
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                                                                                                                                                                                                                  standard; cDNA;
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ilarity 100.0%;
Conservative
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                  Location/Qualifiers
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0; Mismatches
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Pred. No.
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1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        1 BB
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                                                                                                                                                                                                                                                                                                                                                                                                                      .4e+02;
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RESULT
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Best Local S
Matches 12
JO8089249-A.
09-ADR-1996, 234612.
29-SEP-1994, JP-234612.
29-SEP-1994, JP-234612.
(MITU ) MITSUBISHI CHEM C
WPI; 96-23342/24.
P-PSDB; R91947.
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18-JAN-1995.
11-JUL-1994;
12-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyro:phosphorylase

Disclosure; Page 21-24; 35pp; English.

Disclosure; Page 21-24; 35pp; English.

The sequence represents a potato tuber ADP-glucose-pyrophosphorylase small subunit gene. The gene is modified by site-directed mutagenesis to include a BglII-NcoI site at the ATG codon, a SacI site at the stop codon, and an internal BglII site is removed. A methionine initiation codon is introduced for expression of the mature protein in Escherichia coli. The gene is cloned together with the large subunit gene (094439) (on compatible plasmids), and subjected to mutagenesis to give improved variants of the enzyme. The resulting variant genes may be expressed in an oilseed crop plant to reduce the oil content in seeds, for use in feedstuff and food recolute.
                                                                                                                                                                                                                                                                                     27-NOV-1996 (first entry)
Brevibacterium flavum MJ-233 dihydroxy acid dehydratase coding region Dihydroxy-acid dehydratase; EC 4.2.1.9; amino acid biosynthesis; isoleucine; Ile; valine; Val; Corvneform hartning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn of seeds e.g. peanut or soybean having decreased oil content - by providing increased levels of ADP glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barry GF, Kishore GM,
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                                                                                                                                                                                                                        mat_peptide
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ence 1575
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12; Conserv
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US-090523.
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/note= "site for i
(primer Q85018)"
234. .435
234. .435
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/note= "EC-2.7.7.27"
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/EC_number=
                                                                                                                                                                                                                                            Location/Qualifiers
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                                                       CORP
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Pred. No.
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1.4e+02;
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Matches 12
                                                                                                                                        DNA fragment contg. a gene coding for di:hydroxy-acid dehydratase derived from Brevibacterium flavum MJ 233, useful for prodn. of L-isoleucine and L-valine Claim 5; Page 9-11; 12pp; Japanese. A 6 kb genomic DNA KpnI fragment containing an open reading frame (ORF) coding for dihydroxy-acid dehydratase was isolated from Brevibacterium flavum MJ-233. The sequence of the 1836 bp ORF was determined (i.e. the present sequence) and was found to encode a protein of 612 amino acids. The enzyme is involved in biosynthesis of the amino acids isoleucine and valine.

Sequence 1836 BP; 426 A; 606 C; 475 G; 329 T;
   438
l Similarity
12; Conserv
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   449
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Pred. No.
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Search completed: September 12, 2000, 23:07:26 Job time: 4108 sec

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Title:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-460-741-1
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US-08-90-523-7
US-08-398-627-7
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PCT-US94-05275-7
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US-08-376-843-2
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APPLICATION APPLICATION FILING DATE: CLASSIFICATIO ATTORNEY-AGENT NAME: Sholtz REGISTRATION REFERENCE/DOC TELECOMMUNICATI TELEPAX: (41 TELEPAX: (41 TELEPAX: (41 TELEPAX: (31) TYPE: nucled STRANDEDNESS: TOPOLOGY: 11 MOLECULE TYPE: HYPOTHETICAL: NOTI-SENSE: NO	T 1 1 - 592-126/c uence 126, App ent No. 582109 MERAL INFORMAT TITLE OF INVEN TITLE OF INVEN UMBER OF SEQU CORRESSEE: ADDRESSEE: ADD	
APPLICATION NUMBER: US/08/5 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615 REFERENCE/DOCKET NUMBER: 46 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0980 TELEFAX: (415) 324-0980 TELEFAX: (415) 324-0960 FORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS: LENGTH: 319 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO	SULT 1 -08-592-126-126/c -08-592-126 Application US Sequence 126, Application US Sequence 126, Application US Sequence 126, Application US Sequence 126, Application US PATENT INFORMATION: Tran TITLE OF INVENTION: Tran TITLE OF INVENTION: Poly NUMBER OF SEQUENCES: Poly NUMBER OF SEQUENCES: Poly CORRESPONDENCE ADDRESS: ADDRESSEE: Dehlinger & STREET: 350 Cambridge CITY: Palo Alto STREET: GA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: IEM PC compa OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel- COMPUTERE: TAM PC compa OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel- COMPUTERE: TAM PC compa	88 887
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US/08 US/08 TION: as K. as K. 38,6 as R. 4-0880 0960 0960 0960 09 12 25: 12 5 mRNA	on US/08 Dolganov Transcr Polypep 153: SS: 1649e Ave idge Ave py disk compatib pC-DOS/ DREADAA.	
US/08/592,126 US/08/592,126 ION: S K. S K. S K. HONE HOROLOMATION: -0880 960 126: S: TS TS	SULT 1 -08-592-126-126/c sequence 126, Application US/08592126 Patent No. 5821091 GENERAL INFORMATION: APPLICANT: Gregory Dolganov TITLE OF INVENTION: Transcripts Encoding Immunomodulatory TITLE OF INVENTION: Polypeptides NUMBER OF SEQUENCES: 151 CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associates STREET: 350 Cembridge Avenue, Suite 250 CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	US-08-049-061-23 US-08-594-031-109 US-08-594-031-115 US-08-694-031-115 US-08-63-115-10 US-08-65-388-10 US-08-465-388-10 US-08-465-388-11 US-08-312-993-11 US-08-312-870-4 US-08-312-870-4 US-08-469-667-8 PCT-US95-07289-8 US-08-468-012A-1 US-08-476-993-3 US-08-477-103-15 US-08-477-103-15 US-08-136-993-8
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RESULT 3
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Sequence 1, Application US/08458077
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APPLICANT: Lyman, Stewart D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple S
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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Carpenter, Melissa
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US-08-458-077-1
Sequence 1, Application US/08460741 Patent No. 5670625
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0
TELEFAX: (206) 233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 01-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
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                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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STREET: Seattle
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NUMBER OF SEQUENCES:
                                                                                        413 CCAATGGAAGCC 424
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                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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OPERATING SYSTEM: Apple S
                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Baum, Peter R
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Microsoft Word for Apple, Version 5.1a
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73..1038
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                                                                                                                                                 92.3%; Score 12;
100.0%; Pred. No.
tive 0; Mismatch
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R

APPLICANT: APPLICANT:

Carpenter, Melissa

STATE: Washington

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RESULT 5
US-08-747-240-1
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US-08-460-741-1
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Best Local Similarity 100.
Watches 12; Conservative
                                                                                                                              Sequence 1, Applic
Patent No. 572881:
GENERAL INFORMAT
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APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTROBUEV ASSETS
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NAME: Seese, Kathryn A.
RECISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
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                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                         FITLE OF INVENTION:
                                                                                                   APPLICANT:
                                                                                                                 APPLICANT:
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OPERATING SYSTEM: Apple St
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              ADDRESSEE:
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                                                                                                                            INFORMATION:
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                                                                                                                                                       Application US/08747240
E: Immunex Corporation
51 University Street
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Baum, Peter R
Carpenter, Melissa
                                                                                                            Lyman, Stewart D.
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100.0%; Pr
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                                            No. 5728813el Cytokine Designated elk Ligand
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                                                                                                  Patricia
                                                                                                                                                                                                                                                                                                  Score 12;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Green
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 587-0430
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FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
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OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
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                                                                     ZIP: 63198
                                                                                                       COUNTRY:
                                                                                                                                       STATE: Missouri
                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                     E: Grace L. Bonner, Monsanto Co. BB4F
700 Chesterfield Parkway No. 5498830th
                                                                                                           USA
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73..1038
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FILING DATE:

18-JUN-1990

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08398627 Patent No. 5608149
                                          APPLICATION NUMBER: US/08/398,627
FILING DATE: 03-MAR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,523
APPLICATION NUMBER: US 07/709663
APPLICATION NUMBER: US 07/709663
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INFORMATION FOR SEQ ID NO: 7:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barry, G
APPLICANT: Kishore,
APPLICANT: Stark, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Enhanced Starch Biosynthesis NUMBER OF SEQUENCES: 51
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LOCATION:
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                                 FILING DATE:
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                                                                                                                                                                                                                                                                     63198
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nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                 St. Louis
: Missouri
                                                                                                                                                                                                                                                                                                                                  E: Grace L. Bonner, Monsanto Co. BB4F
700 Chesterfield Parkway No. 5608149th
                                                                                                                                                                                                                                                                                                                                                                                                                                                Barry, Gerard F.
                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                               Kishore, Ganesh M.
Stark, David M.
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                               07-JUN-1991
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US 07/539763
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Patent No. 5648249
GENERAL INFORMATI
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Best Local :
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
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APPLICANT: Kishore, Ganesh
APPLICANT: Stark, David M.
APPLICANT: Zalewski, James
                                                                                                                           APPLICATION NUMBER: US 08/070,155
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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TITLE OF INVENTION: Method of Improving the Quality of TITLE OF INVENTION: Stored Potatoes
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TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                         REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US94/05275
FILING DATE: 18-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Missouri
                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                            NAME: Bonner, Grace L. REGISTRATION NUMBER:
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12; Conserv
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US-08-406-858-7
RESULT
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; LOCATION:
PCT-US91-04036-7
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PCT-US91-04036-7/c
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32706
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7357
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application PC/TUS9104036 GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
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Best Local :
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Best Local Similarity
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MCB11de, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                              TYPE: NUCLEIC ACID STRANDEDNESS: doub TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19910
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STRANDEDNESS: doub
TOPOLOGY: linear
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12; Conserv
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: Missouri
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700 Chesterfield Village Parkway
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                                                                                       92.3%; 50-
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Increased Starch Content
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                                                                                         Score 12; DB ; Pred. No. 1.2 0; Mismatches
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Pred. No
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hes 0;
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PCT-US94-05275-7
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; Sequence 7, Application PC/TUS9405275
; GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-MAY-1993 INFORMATION FOR SEQ ID NO: 7
FILING FACTOR 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,211
APPLICATION NUMBER: 16-NOV-1990
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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LENGTH: 1575 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Morgan, Robin Wilson
APPLICANT: Willemse, Martha Jacoba
APPLICANT: Claessens, Johannes Antonius Joseph
APPLICANT: Sondermeijer, Paulus Jacobus Antonius
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CITY: Rockville
STATE: Maryland
                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 20850
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1575;
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TELEPHONE: (301)258-5

258-5200

TELECOMMUNICATION INFORMATION:

NAME: Donna Bobrowicz REGISTRATION NUMBER:

32,196

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LOCATION: 14.2005
OTHER INFORMATION:
US-07-912-015-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-468-036-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08468036 Patent No. 5728806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                           TELEX: 25-3856
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/11 APPLICATION NUMBER: US 08/11 FILING DATE: 21-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: NO. 5728006and, Greta REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1224 CCCAATGGAAGC 1213
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCE ADDRESS:

CORRESPONDENCE ADDRESS:

'The second of the second of the
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DeMaggio, APPLICANT: Hoekstra,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 06-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cccaatggaagc 12
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                                                                     ENGTH:
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                                nucleic acid
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: United States of
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                                                                 2625 base pairs
                                                                                                                                                                                                             312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marek's disease herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merl F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/184,605
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. 1.3e+02;
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                                                                            ; NAME/KEY:
; LOCATION:
US-08-376-843-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-376-843-2
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Query Match
Best Local Similarity 100.
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Best Local
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                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5846764and, Gr
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                 TELEFAX: 51.,
TELEFAX: 25-3856
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                                                                                                                                                                                                                               TELEPHONE: 312/7-.
TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300
CITY: Chicago
                                                                                                                                               TOPOLOGY:
                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                       LENGTH:
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12; Conser
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                                                                                                                                                                           nucleic acid
                                                                                                                                                                                     2625 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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                                                                                           CDS
796..2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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796..2580
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                                                                                                                                 DNA (genomic)
                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%;
100.0%;
                       92.3%; Score 12; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anthony J. Merl F.
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lower, 233
                                                                                                                                                                                                                                                                                             35,302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerstein, Murray & Borun
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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1.3e+02;
                                      DВ
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                                      Length 2625;
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US-08-008-216-19
; Sequence 19, Applicat:
; Patent No. 5366887
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Agrobacterium rhizogenes
STRAIN: STRAIN A4
IMMEDIATE SOURCE:
LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
CLONE: CLONE 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (937..2262)
OTHER INFORMATION: /label= ORF1SUBSEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 236-1048
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DALL. 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/725,368
APPLICATION NUMBER: 22-APR-1985
                                                                                                 NAME/KEY: misc_feature
LOCATION: complement (4041..4400)
OTHER INFORMATION: /label= ORF4SUBSEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tepfer, David A.
TITLE OF INVENTION: Ri T-DNA Promoters
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Barnhorst, Marnie W.
REGISTRATION NUMBER: 36,740
REFERENCE/DOCKET NUMBER: P1020US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,216
FILING DATE: 25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       FEATURE:
                                NAME/KEY: misc_feature
LOCATION: complement (4607..4918)
OTHER INFORMATION: /label- ORFSSU
                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: complement (2649..3458)
OTHER INFORMATION: /label= ORF2SUBSEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21126 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 3726..4799
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NAME/KEY: mlsc_feature
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1 B Street, Suite 1700
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                                                                                                                                                                                                         /label- ORF3SUBSEQUENCE
                                         ORF5SUBSEQUENCE
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US-08-459-569-19; Sequence 19, Application US/08459569; Patent No. 5543501
                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label- ORF18SUBSEQUENC
US-08-008-216-19
                                                                                                                            Db 19549 CCAATGGAAGCC 19560
                                                                                                                                                                                                    Query Match 92.3%;
Best Local Similarity 100.0%;
Matches 12; Conservative
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FEATURE:
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LOCATION: complement (5071..5643)
OTHER INFORMATION: /label- ORF7SUBSEQUENCE
FEATURE:
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OTHER INFORMATION: /label- ORF6SUBSEQUENCE FEATURE:
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LOCATION: 15659..16210
OTHER INFORMATION: /label- ORF14SUBSEQUENC
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LOCATION: complement (10509..11282)
OTHER INFORMATION: /label= ORF11SUBSEQUENC
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LOCATION: complement (6576..6830)
OTHER INFORMATION: /label= ORF9SUBSEQUENCE
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LOCATION: 6609..88
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (18177..18743)
OTHER INFORMATION: /label- ORF17SUBSEQUENC
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LOCATION: complement (17737..18189)
OTHER INFORMATION: /label= ORF16SUBSEQUENC
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LOCATION: complement (16517..17545)
OTHER INFORMATION: /label- ORF15SUBSEQUENC
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LOCATION: 13723..14319
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LOCATION: 12466..13002
OTHER INFORMATION: /label-
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LOCATION: complement (
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9748..10044
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6609..8888
PRMATION: /label= ORF8SUBSEQUENCE
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                                                                                                                                                                                                        Score 12; DB 1; I; Pred. No. 1.7e+02; 0; Mismatches 0;
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                                                                                                                                                                                                                                              Length 21126;
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                                                                                                                                                                                                          0
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GENERAL INFORMATION:

0

APPLICANT: Slightom, Jerry L.
APPLICANT: Tepfer, David A.
TITLE OF INVENTION: Ri T-DNA Promoters
NUMBER OF SEQUENCES: 19

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY, CARY, AMES & FRYE

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TELEFAX: (619) 230 ...
TELEFAX: (619) 230 ...
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21126 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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EILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,216
EILING DATE: 25-JAN-1993
APPLICATION NUMBER: US 06/725,368
EILING DATE: 22-APR-1985
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 3726..4799
OTHER INFORMATION: /labe
FEATURE:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Barnhorst, Marnie W.
REGISTRATION UNMBER: 36,740
REFERENCE/DOCKET NUMBER: P1020US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                         NAME/KEY: misc_feature LOCATION: 5143.6216 OTHER INFORMATION: /lak FEATURE:
                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: complement (4607.
OTHER INFORMATION: /label= (
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                                      FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Agrobacterium rhizogenes
STRAIN: STRAIN A4
IMMEDIATE SOURCE:
LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: complement (2649) OTHER INFORMATION: /label=
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LOCATION: complement (937..2262)
OTHER INFORMATION: /label= ORF1SUBSEQUENCE
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CITY: San Diego
STATE: California
                                                                             NAME/KEY: misc_feature
LOCATION: complement (5071..5643)
OTHER INFORMATION: /label= ORF7SUBSEQUENCE
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LOCATION: complement (4
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OTHER INFORMATION:
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WATION: /label= ORF4SU
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6609..8888
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/label= ORF8SUBSEQUENCE
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Search completed: September 12, 2000, 23:04:42 Job time: 3949 sec

Gaps

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QΥ
Db 19549 CCAATGGAAGCC 19560
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                                                                        Query Match
Best Local S
Matches 12
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NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY: misc_feature
LOCATION: 15659..16210
OTHER INFORMATION: /label= ORF14SUBSEQUENC
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LOCATION: complement (6576.
OTHER INFORMATION: /label-
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OTHER INFORMATION: /label- ORF10SUBSEQUENC
FEATURE:
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LOCATION: complement (16517..17545)
OTHER INFORMATION: /label= ORF155UB
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LOCATION: complement (18177...18743)
OTHER INFORMATION: /label= ORF17SUBSEQUENC
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LOCATION: complement (17737..18189)
OTHER INFORMATION: /label= ORF16SUBSEQUENC
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LOCATION: complement (10509..11282)
OTHER INFORMATION: /label= ORF11SUBSEQUENC
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                                                                  ch 92.3%; Score 12; DB 1; I
1 Similarity 100.0%; Pred. No. 1.7e+02;
12; Conservative 0; Mismatches 0;
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12466..13002
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label- ORF9SUBSEQUENCE
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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         em_est1: *
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SUMMARIES

AV281774 AW324305

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the number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.
c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE similar to TR:080828 080828 HYPOTHETICAL 88.8 KD
                                                                                                                                                                                                                                R19461 yg25h04.r1
AW676321 833002H10
R17042 yf45f05.r2
AA788418 r7h07a1.f
AA639559 ng91f08.s
AI273585 q160g11.s
AI093637 ou83d11.s
AI093637 ou83d11.s
AQ062888 nbxb0051M
AQ208746 HS_3229.A
AI1050032 an31a04.x
AW136253 UI-H-BI1-AQ019463 UI-H-BI1-AQ019463 CIT-HSP-2
AI367860 gq45f05.x
AI123505 qa01g08.x
AQ065876 nbeb0022x
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D69385 CELK069E9F
D69385 CELK073EYF
AA785620 g9f05a1.f
AW025820 wv08c09.x
AW028366 wv08b03.x
B63027 CIT978SK-13
AW442811 EST307741
AA966772 s9b01a1.f
A102536 ow58b03.s
AA570786 nm37e03.s
AA570788 m37e03.s
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AW324305 U27301:
AW38698 AV386980
AV278622 AV278622
AA282475 zs90c01:
AW698136 UXNV_073
N28122 MDB1422R MO
A1352128 GY10f07:
AW411422 fhl2c03:
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AW411424 fhl2c03:
AW411427 fhl1a1:
A1845473 UI-M-A01-
A1043778 UI-M-F.01-
A1043778 UI-M-F.01-
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AI379962
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AUTHORS
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Klanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project
Unpublished (1999)
On Jan 6, 2000 this sequence version replaced gi:6675643.
Contact: Shoemaker R/Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Email: lone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems or
    mRNA sequence.
AI379962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: SHOWMENT Project
Public Soybean EST Project
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN. ;, mRNA sequence.
AW396623
AW396623.1 GI:6915162
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                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly(dT) primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT7T3-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pT7T3-Pac (Pharmacia); Site_1: EcoRI
Site_2: HindIII; This cDNA library was constructed
mRNA isolated from senecsing leave tissue of mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Senescing leaves, mature plants, greenhouse
grown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="GENOME SYSTEMS CLONE ID: Gm-c1026-44"
/clone_lib="Gm-c1026"
                                       175 bp ml
1 NCI_CGAP_CLL1 l
5 SW:UCRP_HUMAN l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glycine max"
/db_xref="taxon:3847"
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eudicotyledons; Rosidae; eurosids I; Fabales;
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                                                                                                                                                                                                                                                                                 Score 13; DB 71;
Pred. No. 7.8e+02;
; Mismatches 0;
                                         mRNA EST 18-MAR-1999
Homo sapiens cDNA clone IMAGE:2072531
P05161 UBIQUITIN CROSS-REACTIVE PROTE
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                                                                                                                                                                                                                                                                                                                        Length 164;
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                                              PROTEIN
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RESULT 1 AW396623/c DEFINITION

AW396623 sg80d10.y1 G Gm-c1026-44

l Gm-c1026 14 5' simil

164 bp

mRNA

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AQ019463 AI367860

AW136253 AW137518 AQ208746 AI050032 000 O O C

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AA785620 AW025820 AW028366

AA570786 AZ037328 AW442811 AA966772 AI022536

R19461

AA788418 AA639559 AW676321 R17042 იი

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AV386986 AV278622 AA282475 AW698136 N28122 AA1352128 AW411422 AA786244 AI1845473 AI1043778

COMMENT

TITLE

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SOURCE
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AUTHORS
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Best Local
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45 CCCAATGGAAGCC 57
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Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.linl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                         AV281774 189 bp mRNA EST 05-NOV-1999 AV281774 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus CDNA clone 4933426F15 3', mRNA sequence.
AV281774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137165
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 189)
                                                                                                                                                                                                     Mus musculus
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Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.
                                                                                                                                                                                                                                                                                                                                      AV281774.1
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                                                                                                                                                                                                                                                         house mouse.
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/Clone_lib="NCI_CGAP_CLL1"
/Clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="0H10B"
/lab_host="0H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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/db_xref="taxon:9606"
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Pred. No.
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. 7.9e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 175;
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1 cccaatggaagcc

Query Match Best Local

Matches

1 Similarity 100

100.0%;

Score 13; Pred. No. Mismatches

8e+02; DB 60; 0

Length 189; Indels

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Gaps

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawaki,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., On,Apr. 7, 1998 this sequence version replaced gi:3034900.
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URL:http://genome-rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                      65
                                    contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGAGACTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was contributed by the contributed 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="4933426F15"
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/dev_stage="adult"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Other_ESTs: uo27a01.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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AW324305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
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                                                    AV386986 215 bp mRNA EST 21-JAN-2000 AV386986 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CMO10g1l_r, mRNA sequence.

AV386986
Chlamydomonas reinhardtii
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10000"
/clone=_TrWAGE:_5616072"
/clone__lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salsite_2: NotI; Cloned unidirectionally. Primer: Oligo c Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" 40 c 54 g 50 t
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Pred. No. 8.1e+02;
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                                                                                                                                                                     RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Nilsel (1999)

AL Unpublished (1999)

On Jul 8, 1999 this sequence version replaced gi:5420947.

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, The Institute of Physical and Chemical Research (RIKEN), Genomic
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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AV278622 RIXEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4933402018 3', mRNA sequence.
AV278622
                                   3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Mammalia; Eutheria;
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genome-res@rtc.riken.go.jp,
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/clone="Chlamydomonas reinhardtii C9"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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/strain="C9"
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Rodentia;
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 254)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                          zs90c01.s1 NCI_CGAP_GCB1 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai, T., Akiyama J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL:http://genome.rtc.riken.go.jp/Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Matahiki,M., Okazaki,Y. and Matauura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                              EST
                                                                              Homo sapiens
                                                                                                                                                                                        AA282475
                                                                                                                           AA282475.1 GI:1925437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details.
                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="4933402018"
/clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ви10в)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                        254 bp
                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                 0:
                                                                                                                                                                                                                                                                                                                             Score 13; DB 59;
Pred. No. 8.3e+02;
Mismatches 0;
                                                                                                                                                                                         mRNA
                                                                                                                                                                         Ното
                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      EST 13-AUG-1997 sapiens cDNA clone IMAGE:704736
 Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                              Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
On Jan 14, 1998 this sequence version replaced
                                                                                            Contact: Johnson, Arthur
North Carolina State University
Tel: 919 915 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                            AW698136 293 bp mRNA
NXNV_073_C07_F Nsf Xylem Normal wood
Clone NXNV_073_C07 5', mRNA sequence.
                                                                                                                                            Unpublished (2000)
                                                                                                                                                                      Sederoff, R.
                                                                                                                                                                               Coniferopsida; Coni
1 (bases 1 to 293)
                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Trach
Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                    Pinus taeda
                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                     AW698136
                                                                                                                                                        Molecular Basis of Wood Formation
                                                                                                                                                                                                                                                         AW698136.1 GI:7580722
                                                                                Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                  lobiolly pine.
                                                                      primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="NxW_073_C07"
/clone_11b="Nsf Xylem Normal wood Vertical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:704736"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"taxon:9606"
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                                                          ocation/Qualifiers
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Pred. No.
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να. No. 8.4e+02;
Mismatches
                                                                                                                                                                                                                                                                                        mRNA EST 17
Normal wood Vertical Pinus
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                                                                                                                                                          the Pine Megagenome
                                                                                                                                                                                                       Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 254;
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Best Local S
Matches 13
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Best Local S
Matches 13
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                                                                                                                                                                                                                                34 CCCAATGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cccaatggaagcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse brain cDNAs (1995) upublished (1995) (1995) may 14, 1999 this sequence version replaced gi:4827793. Contact: Sikela JM Department of Pharmacology University of Colorado Health Sciences Center Box C236, 4200 E. 9th Ave, Denver CO 80262-0236 Tel: 3032708637
                    AI352128 326 bp mRNA EST 13-FEB-1999 gr10f07.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1940485 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nikki@tally.uchsc.edu
Insert Length: 403 Std Error:
Seq prlmer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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N28122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:1090"
/dlow_ref="taxon:1090"
/clone_lib="Mouse brain, Stratagene"
/lab_host="E. coli XIJ-Blue"
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
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/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="vector: Lambda ZAP; Site_1: Lamb
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a 67 c 60 g 83 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:1145978
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            Score 13; DB 86;
Pred. No. 8.6e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 80;
Pred. No. 8.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.00
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RESULT 11
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KEYWORDS
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13; Conserv
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1 (bases 1 to 326)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 332)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                      Unpublished (1999)
On Apr 30, 1999 this sequence version Contact: Robert Strausberg, Ph.D.
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fh12c03.y1 NIH_MGC_17 Homo
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                                                                       Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 81 c 75 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="INAGE:1940485"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 8.8e+02;
No. Wismatches 0;
                                                                                                                                                                                                                                                                                                                                        sapiens cDNA
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                                                                                                        replaced gi:4727490
                                                                                                                                                                                                                                                                                                                                          EST 16-FEB-200 clone IMAGE:2964485
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                  Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo, Prade,R. and Roe,B.
An Aspergillus nidulans EST Database
Unpublished (1998)
Other_ESTs: J7hllal.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklaho
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus nidulans
Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
anamorphic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA786244 338 bp mRNA EST 31-JUL-1998

J7hilal.fl Aspergillus nidulans 24hr asexual developmental and

vegetative cDNA lambda zap library Aspergillus nidulans cDNA clone

J7hilal 3', mRNA sequence.
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Plate: LLAM64 row: F column: 6
Seq primer: M13RP1 reverse primer (ABI).
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                           Email: broe@ou.edu
We anticipate the future release
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                   Parrington Oval,
: 405 325 4912
: 405 325 7762
                                                                                                                                                                                            primer: M13-20
                                                                                                                                                                   quality sequence stop: 307
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/lab_host-"plf108 (phage-resitant)"
/lab_host-"plf108 (phage-resitant)"
/note-"organ: muscle; vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming the
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG(). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of Callfornia, Berkeley) using ZAP-cDNA synthesis kit
(Strategene) and Superscript II RT (Life Technologies)."
a 70 c 46 g 141 t
                                                                                                                                           Location/Qualiflers
                                            /organism="Aspergillus nidulans"
/strain="FGSC A26"
/db_xref="taxon:5072"
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/clone_lib="NIH_MGC_17"
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/db_xref="taxon:9606"
/clone-"j7hllal"
/clone_lib-"Aspergillus nidulans 24hr asexual
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. 8.8e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                         University of Oklahoma
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:
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UI-M-AO1-aej-h-05-0-UI.sl NIH_BMAP_MPG_N Mus musculus cDNA clone
UI-M-AO1-aej-h-05-0-UI 3', mRNA sequence.
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1 (bases 1 to 338)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20892-9643, USA
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/organism="Mus musculus"
/organism="Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/db_xref="UrM-Aol-ae]-h-05-0-UI"
/clone="Ib="NIH_BMAP_MPG_N"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental and vegetative cDNA lambda zap library*
//tissue_type="vegetative mycelia, asexual structures*
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript
a 86 c 68 g 91 t l others
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Pred. No. 8.8e+02;
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Genome Research 6:

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UI-R-CO-jm-f-10-0-UI.s', mRNA sequence.
AI043778.1 GI:3290513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult 8-Day-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID-178:157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 348)
Bonaldo, M.F., Lennor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jun 5, 1998 this sequence version replaced gi:3189294 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Forward POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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//dev_stage="adult"
//dev_stage="adult"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            791-806, 1996. Tissue provided by Ms. Annie Novakovich, zivic-Miller Laboratories.; TAG_LIB=NIH_BMAP_MPG_N; TAG_TISSUE=pineal-glands; TAG_SEQ=CAGAC" 84 g 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-jm-f-10-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="UI-R-C0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
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. 8.8e+02;
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                                  1 cccaatggaagcc 13
CCCAATGGAAGCC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 350)
1 (bases 1 to 350)
1 (Combie, W.R., Kelley, J.M., Aubin, L., Goscoechea, M., FitzGerald, M.G., Wu, A., Adams, M.D., Dubnick, M., Kerlavage, A.R., Venter, J.C. and Fields, C.A.
Caenorhabditis elegans cDNAs
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic 9712 Medical Center Drive, rel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wEST01614 Early embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T00893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 5, 1995 this sequence version replaced g1:798322 Other_ESTs: wEST01615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T00893.1 GI:277374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans cDNA clone CEESK50,
                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
Insert Length: 1663 Sto
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 3018699423
                                                                                                Similarity
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                                                                                                                                                                                            89
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UT-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="CEBSK50"
/clone="CEBSK50"
/clone_lib="Early embryo, Stratager
/clone_172 g 84 t 2
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 8.9e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
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                                                                                                    Score 13; DB 89;
Pred. No. 8.9e+02;
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                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Research
Rockville,
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                                                                                                                          DB 89;
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                                                                                                                      Length 350;
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                                                                                      Indels
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